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(54) Title: **NOGO RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH**

(57) Abstract: Disclosed are NgR proteins and biologically active Nogo (ligand) protein fragments. Also disclosed are compositions and methods for modulating the expression or activity of the Nogo and NgR protein. Also disclosed are peptides which block Nogo-mediated inhibition of axonal extension. The compositions and methods of the invention are useful in the treatment of cranial or cerebral trauma, spinal cord injury, stroke or a demyelinating disease.



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**NOGO RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH****INVENTOR**

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**CROSS-REFERENCE TO RELATED APPLICATIONS**

This application is a continuation-in-part of U.S. application 09/758,140, filed January 12, 2001, which claims benefit from U.S. Provisional Patent Applications 60/175,707 filed January 12, 2000; 60/207,366 filed May 26, 2000; 10 60/236,378 filed September 29, 2000 which are herein incorporated by reference in their entirety. This application is also a continuation-in-part of international application PCT/US01/01040, filed January 12, 2001.

**U.S. GOVERNMENT SUPPORT**

15 This invention was partially made with government support under National Institute of Health Grant RO1-NS 33020, RO1-NS39962 and RO1-NS42304.

**FIELD OF THE INVENTION**

The invention relates to neurology and molecular biology. More 20 particularly, the invention relates to CNS neurons and axonal growth

**BACKGROUND OF THE INVENTION**

Axons and dendrites of neurons are long cellular extensions from neurons. At the distal tip of an extending axon or neurite is a specialized region, known as the 25 growth cone. Growth cones are responsible for sensing the local environment and moving toward the neuron's target cell. Growth cones are hand shaped, with several long filopodia that differentially adhere to surfaces in the embryo. Growth cones can be sensitive to several guidance cues, for example, surface adhesiveness, growth factors, neurotransmitters and electric fields. The guidance of growth at the cone

depends on various classes of adhesion molecules, intercellular signals, as well as factors which stimulate and inhibit growth cones. The growth cone located at the end of a growing neurite advances at various rates, but typically at the speed of one to two millimeters per day. The cone consists of a broad and flat expansion, with numerous  
5 long microspikes or filopodia that extend like spikes. These filopodia are continually active. While some filopodia retract back into the growth cone, others continue to elongate through the substratum. The elongations between different filopodia form lamellipodia.

The growth cone can explore the area that is ahead of it and on either side with  
10 its lamellipodia and filopodia. When an elongation comes in contact with a surface that is unfavorable, it withdraws. When an elongation comes into contact with a favorable surface, it continues to extend and can manipulate the growth cone moving in that direction. Hence, the growth cone can be guided by small variations in surface properties of the substrata. When the growth cone reaches an appropriate target cell a  
15 synaptic connection is created.

Damaged neurons do not regenerate in the central nervous system (CNS) following injury due to trauma and disease. The absence of axon regeneration following injury can be attributed to the presence of axon growth inhibitors. These inhibitors are predominantly associated with myelin and constitute an important barrier  
20 to regeneration. Axon growth inhibitors are present in CNS-derived myelin and the plasma membrane of oligodendrocytes, which synthesize myelin in the CNS (Schwab *et al.*, (1993) *Ann. Rev. Neurosci.* 16, 565-595).

CNS myelin is an elaborate extension of the oligodendrocyte cell membrane. A single oligodendrocyte myelinates as many as thirty different CNS axonal segments.  
25 Oligodendrocyte membrane extensions wrap around the axons in a concentric fashion to form the myelin sheath. Tightly compacted mature myelin consists of parallel layers of bimolecular lipids apposed to layers of hydrated protein. Active myelin synthesis starts *in utero* and continues for the first two years of human life. Slower synthesis continues through childhood and adolescence while turnover of mature myelin

continues at a slower rate throughout adult life. Both developing and mature forms of myelin are susceptible to injury from disease or physical trauma resulting in degradation of the myelin surrounding axons.

Myelin-associated inhibitors appear to be a primary contributor to the failure of  
5 CNS axon regeneration *in vivo* after an interruption of axonal continuity, while other non-myelin associated axon growth inhibitors in the CNS may play a lesser role. These inhibitors block axonal regeneration following neuronal injury due to trauma, stroke, or viral infection.

Numerous myelin-derived axon growth inhibitors have been characterized  
10 (see, for review, David *et al.*, (1999) WO9953945; Bandman *et al.*, (1999) U.S. Patent 5,858,708; Schwab, (1996) Neurochem. Res. 21, 755-761). Several components of CNS white matter, NI35, NI250 (Nogo) and Myelin-associated glycoprotein (MAG), which have inhibitory activity for axonal extension, have been also been described (Schwab *et al.*, (1990) WO9005191; Schwab *et al.*, (1997) U.S. Patent 5,684,133). In  
15 particular, Nogo is a 250 kDa myelin-associated axon growth inhibitor which has been cloned and characterized (Nagase *et al.*, (1998) DNA Res. 5, 355-364; Schwab, (1990) Exp. Neurol. 109, 2-5). The Nogo cDNA was first identified through random analysis of brain cDNA and had no suggested function (Nagase *et al.*, (1998) DNA Res. 5, 355-364).

20 Schwab and colleagues published the sequence of six peptides randomly derived from a proteolytic digest of presumed bovine NI250 (Nogo) protein (Spillmann *et al.*, (1998) J. Biol. Chem. 273, 19283-19293). A probable full-length cDNA sequence for this protein was recently deposited in the GenBank. This 4.1 kilobase human cDNA clone, KIAA0886, is derived from the Kazusa DNA Research  
25 Institute effort to sequence random high molecular weight brain-derived cDNA (Nagase *et al.*, (1998) DNA Res. 31, 355-364). This novel cDNA clone encodes a 135 kDa protein that includes all six of the peptide sequences derived from bovine Nogo.

The human Nogo-A sequence shares high homology over its carboxyl third



with the Reticulon (Rtn) protein family. Rtn1 has also been termed neuro-endocrine specific protein (NSP) because it is expressed exclusively in neuro-endocrine cells (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416). All Rtn proteins share a 200 amino acid residue region of sequence similarity at the carboxyl terminus of the protein (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416; Roebroek *et al.*, (1996) Genomics 32, 191-199; Roebroek *et al.*, (1998) Genomics 51, 98-106; Moreira *et al.*, (1999) Genomics 58, 73-81; Morris *et al.*, (1991) Biochim. Biophys. Acta 1450, 68-76). Related sequences have been recognized in the fly and worm genomes (Moreira *et al.*, (1999) Genomics 58, 73-81). This region is approximately 70% identical across the Rtn family. Amino terminal regions are not related to one another and are derived from various alternative RNA splicing events.

From analysis of sequences deposited in the GenBank and by homology with published Rtn1 isoforms, three forms of the Nogo protein are predicted (Nogo-A, Nogo-B, Nogo-C). Nogo-B of 37 kDa might possibly correspond to NI35, and explain the antigenic relatedness of the NI35 and NI250 (Nogo-A) axon outgrowth inhibiting activity. Nogo-C-Myc exhibits an electrophoretic mobility of 25 kDa by SDS-PAGE and has been described previously as Rtn4 and vp2015. The ability of Nogo-A protein to inhibit axonal regeneration has been recognized only recently (GrandPré *et al.*, (2000) Nature 403, 439-444; Chen *et al.*, (2000) Nature 403, 434-439; Prinjha *et al.*, (2000) Nature 403, 483-484).

The absence of re-extension of axons across lesions in the CNS following injury has been attributed as a cause of the permanent deleterious effects associated with trauma, stroke and demyelinating disorders. Modulation of NI250 has been described as a means for treatment of regeneration for neurons damaged by trauma, infarction and degenerative disorders of the CNS (Schwab *et al.*, (1994) WO9417831; Tatagiba *et al.*, (1997) Neurosurgery 40, 541-546) as well as malignant tumors in the CNS such as glioblastoma (Schwab *et al.*, (1993) U.S. Patent 5,250,414; Schwab *et al.*, (2000) U.S. Patent 6,025,333).

Antibodies which recognize NI250 have been reported to be useful in the

diagnosis and treatment of nerve damage resulting from trauma, infarction and degenerative disorders of the CNS (Schnell & Schwab, (1990) Nature 343, 269-272; Schwab *et al.*, (1997) U.S. Patent 5,684,133). In axons which become myelinated, there is a correlation with the development of myelin and the appearance of Nogo.

5 After Nogo is blocked by antibodies, neurons can again extend across lesions caused by nerve damage (Varga *et al.*, (1995) Proc. Natl. Acad. Sci. USA 92, 10959-10963).

The mechanism of action whereby Nogo inhibits axonal growth has not yet been elucidated. Identification and characterization of this mechanism of action and the biochemical pathways associated with the effects of Nogo would be useful in

10 treatment of disease states associated with axonal injury and axonal demyelination.

#### SUMMARY OF THE INVENTION

Genes encoding murine and human receptors for Nogo (NgR) have been discovered. Various domains in the NgR polypeptide have been identified, and

15 certain of their functions have been discovered. In addition, important aspects of the interaction of specific regions of the Nogo polypeptide (ligand) with NgR have been discovered. Based on these and other discoveries, the invention features molecules and methods useful for decreasing Nogo-dependent inhibition of axonal growth in CNS neurons.

20 The invention includes a NgR-derived polypeptide that contains amino acid residues 27-309 of SEQ ID NO:2 (human NgR NTLRRCT domain), while containing fewer than 115 consecutive amino acids from amino acids 310-445 of SEQ ID NO:2 (human NgR CTS domain). The NgR NTLRRCT domain optionally includes up to 20 conservative amino acid substitutions. In some embodiments, the encoded

25 polypeptide contains fewer than 50 consecutive amino acids from amino acids from the NgR CTS domain. While the polypeptide may include a functional GPI domain, a functional GPI domain may be absent, e.g., when a soluble polypeptide is desired. The invention also includes a nucleic acid encoding a NgR-derived polypeptide; a vector, e.g., operably linked to an expression control sequence, containing the nucleic

acid; and a transformed host cell containing the vector. The invention also includes a method of producing a NgR-derived polypeptide. The method includes introducing a nucleic acid encoding the above-described polypeptide into a host cell, culturing the host cell under conditions suitable for expression of said polypeptide, and recovering  
5 the polypeptide.

The invention also includes an antibody that binds to an epitope in the CTS domain of NgR. The antibody can be polyclonal or monoclonal.

The invention also includes a method of inhibiting binding of a Nogo polypeptide to a NgR. The method includes contacting the Nogo polypeptide with an  
10 effective amount of the above-described NgR-derived polypeptide.

The invention also includes a method of inhibiting binding of a Nogo polypeptide to a NgR, comprising contacting the NgR with an antibody that binds to the amino acid sequence consisting of SEQ ID NO:2 (NgR polypeptide).

The invention also includes a method of decreasing inhibition of axonal  
15 growth by a CNS neuron. The method includes contacting the neuron with an effective amount of: (a) an above-described NgR-derived polypeptide; or (b) an antibody that binds to the amino acid sequence set forth as SEQ ID NO:2 (NgR). In some embodiments of the invention, the antibody binds to an epitope within the amino acid sequence consisting of amino acids 310-445 of SEQ ID NO:2 (CTS  
20 domain of NgR).

The invention also includes a method of treating a central nervous system disease, disorder or injury, e.g., spinal cord injury. The method includes administering to a mammal, e.g., a human, an effective amount of: (a) an agent that inhibits binding of a Nogo polypeptide to a NgR; or (b) an agent that inhibits  
25 NgR-dependent signal transduction in a central nervous system neuron. Exemplary agents for inhibiting binding of a Nogo polypeptide to a NgR include: (a) an above-described NgR-derived polypeptide; and (b) an antibody that binds to the NgR polypeptide (SEQ ID NO:2). In some embodiments, the antibody binds to an epitope within the CTS domain of NgR (amino acids 310-445 of SEQ ID NO:2).

The invention also includes a method for identifying a molecule that inhibits binding of a Nogo polypeptide to a NgR. The method includes: (a) providing a NgR polypeptide; (b) contacting the NgR polypeptide with a candidate molecule; and (c) detecting a decrease in binding of the Nogo polypeptide to the NgR in the presence of  
5 the candidate molecule, as compared to the binding of the Nogo polypeptide to the NgR in the presence of the candidate molecule.

The method also includes pharmaceutical compositions. In some embodiments the composition contains an above-described NgR-derived polypeptide and a pharmaceutically acceptable carrier. In other embodiments, the composition  
10 contains an antibody that binds to an epitope in the NgR CTS domain, and a pharmaceutically acceptable carrier.

The invention also includes a polypeptide that contains the amino acid sequence IYKGVQAI or EELV, or both, with the polypeptide containing a total of 40 amino acids or fewer ("Nogo ligand-derived polypeptide"). In some embodiments, the  
15 Nogo ligand-derived polypeptide includes amino acid residues 2 to 34 of SEQ ID NO:21. In some embodiments, the Nogo ligand-derived polypeptide includes a heterologous amino acid sequence not present in NogoA, wherein the heterologous amino acid sequence contains at least five amino acid residues. The invention also includes a nucleic acid encoding a Nogo ligand-derived polypeptide; a vector, e.g.,  
20 operably linked to an expression control sequence, containing the nucleic acid; and a transformed host cell containing the vector.

The invention also includes an antibody that binds to an above-described Nogo ligand-derived polypeptide. The antibody can be polyclonal or monoclonal. The invention also includes a composition that contains an above-described  
25 NgR-derived polypeptide and a pharmaceutically acceptable carrier or an antibody that binds to an epitope in the NgR CTS domain, and a pharmaceutically acceptable carrier.

The invention also includes an alternative method of inhibiting binding of a Nogo polypeptide to a NgR. The alternative method includes contacting the Nogo

polypeptide with an effective amount of an above-described Nogo ligand-derived polypeptide.

The invention also includes an alternative method of decreasing inhibition of axonal growth by a CNS neuron. The alternative method includes contacting the  
5 neuron with an effective amount of an above-described Nogo ligand-derived polypeptide.

The invention also includes an alternative method of treating a central nervous system disease, disorder or injury, e.g., a spinal cord injury. The alternative method includes administering to a mammal, e.g., a human, an effective amount of an  
10 above-described Nogo ligand-derived polypeptide.

The invention also includes a method of identifying a molecule that decreases Nogo-dependent inhibition of axonal growth. The method includes: (a) providing a polypeptide containing a target sequence consisting of IYKGVQAI or EELV, or both; (b) contacting the polypeptide with a candidate molecule; and (c) detecting  
15 binding of the candidate molecule to a target sequence in the polypeptide.

The invention also includes embodiments wherein SEQ ID NO:4 (murine NgR) is substituted for SEQ ID NO:2 (human NgR). Those of skill in the art will recognize where the human sequence is preferable over the murine sequence and visa  
20 versa.

## DESCRIPTION OF THE FIGURES

Figure 1 - Comparison of Nogo domains

(a) is a schematic diagram which summarizes features of the Nogo proteins  
25 utilized in this study. (b) is a photograph of NIH-3T3 fibroblasts cultured on surfaces coated with Amino-Nogo, GST-Nogo-66 or no protein and stained for filamentous actin (scale bar, 40  $\mu$ m). (c) is a photograph of chick E12 dorsal root ganglions cultured on surfaces coated with Amino-Nogo, GST-Nogo-66 or no protein (substrate-bound) or with 100 nM Nogo protein (soluble) (scale bar, 40  $\mu$ m). (d) is a

photograph of a gel and an immunoblot where purified Amino-Nogo-Myc-His protein was subjected to SDS-PAGE and stained with Commassie Brilliant Blue (CBB) or immunoblotted with anti-Myc antibodies (Myc) (molecular weight markers of 200, 116, 97, 65 & 45 kDa are at left). (e) is a graph displaying experimental data where the percentage of 3T3 fibroblasts with an area greater than 1200  $\mu\text{m}^2$  (spread) was measured from experiments as in (b) on Nogo-coated surfaces (black) or with soluble 100 nM Nogo preparations (blue) (AM, Amino-Nogo; AM+Myc, Amino-Nogo preincubated with anti-Myc antibody; AM+Myc+Mo, AM+Myc preincubated with anti-mouse IgG antibody; Myc+Mo, anti-Myc antibody plus anti-murine IgG antibody). (f) is a graph displaying experimental data where the percentage of spread COS-7 cells was determined after culture on Nogo-coated surfaces or with soluble 100 nM Nogo preparations. (g) is a graph displaying experimental data where the effects of purified preparations of GST-Nogo-66 or Amino-Nogo on growth cone morphology was assessed in E12 dorsal root ganglion cultures at the indicated concentrations after thirty minutes. This demonstrates that GST-Nogo-66 is two orders of magnitude more potent than Amino-Nogo in this assay. (h) is a graph displaying experimental data where the neurite outgrowth per cell in E13 dorsal root ganglion cultures was quantitated from experiments as in (c) on Nogo-coated surfaces or with soluble 100 nM Nogo preparations. (i) is a graph displaying experimental data where the effects of Nogo preparations on neurite outgrowth in cerebellar granule neurons was measured.

**Figure 2 - Nogo fragments antagonize Nogo and CNS myelin action**

(a) is a photograph of chick E12 dorsal root ganglion explants that were cultured and growth cone collapse assessed as described in Figure 4. Cultures were exposed to the following preparations for thirty minutes before fixation and staining with rhodamine-phalloidin: buffer only (Control); 15 nM GST-Nogo; 1  $\mu\text{M}$  each of Pep1, Pep2 and Pep3 (Pep); 15 nM GST-Nogo plus 1  $\mu\text{M}$  each of Pep1, Pep2 and Pep3 (Nogo + Pep). Note that growth cone collapse by Nogo is blocked by peptide

addition. Pep1, residues 1-25 of the extracellular domain; Pep2, 11-35; and Pep3, 21-45. (b) is a graph quantifying the results from growth cone collapse assays as in (a). Individual peptides were included at 4  $\mu$ M, and the peptide 1-3 mixture was 1  $\mu$ M of each peptide. CNS myelin was prepared as described and the indicated total  
5 myelin protein concentrations were included in the cultures. All results are the means  $\pm$  s.e.m. calculated from four to seven determinations. Those values significantly different from the corresponding values with the same concentration of Nogo or myelin but without peptide are indicated (asterisk,  $p < 0.05$ , Student's two-tailed t test).

10

Figure 3 - Nogo antagonist Pep2-41

(a) is a graph displaying the results of chick E12 dorsal root ganglion growth cone collapse assays. These assays were performed and quantified as in GrandPré *et al.*, (2000) Nature 403, 439-444. Assays were conducted with no addition (Control),  
15 15 nM GST-Nogo or 15 nM GST-Nogo plus 1  $\mu$ M Pep2-41 (Nogo + Pep). The values are means  $\pm$  s.e.m. calculated from four determinations. (b) is a graph displaying the results of binding experiments where binding of 10 nM AP-Nogo to chick E12 dorsal root ganglion neurons was measured as described in Figure 4 with the addition of the indicated concentrations of Pep2-41.

20

Figure 4 - Nogo Pep2-41 prevents both Nogo & CNS myelin inhibition of neurite outgrowth

This figure is a graph which displays the results of outgrowth assays where neurons were cultured in the presence of the indicated concentrations of Pep2-41,  
25 purified GST-Nogo (GST-Nogo-66) protein (a) and crude CNS myelin protein (b). Chick E13 dorsal root ganglion neurons were cultured under standard conditions. For outgrowth assays, neurons were cultured in the presence of the indicated concentrations of Pep2-41, purified GST-Nogo (GST-Nogo-66) protein and crude CNS myelin protein. This demonstrates that Pep2-41 can reverse the inhibition of

neurite outgrowth by either GST-Nogo or total CNS myelin.

**Figure 5 - Ligand binding assay for axonal Nogo receptors**

(a) is a photograph of a gel and an immunoblot where the His-AP-Nogo (66 amino acid) protein was expressed in HEK293T cells, and purified from conditioned medium on a Nickel-containing resin via the His tag. Purified protein was subjected to SDS-PAGE and stained for total protein with CBB or immunoblotted with anti-Nogo antibodies (anti-Nogo). Molecular weight markers of 200, 116, 97, 65 and 45 kDa are shown at left, and the migration of AP-Nogo at right. (b) is a photograph of dissociated chick E12 dorsal root ganglion neurons that were incubated with 10 nM AP-Nogo or 10 nM AP-Nogo + 160 nM GST-Nogo for sixty minutes at 23°C. The cells were washed, fixed and incubated at 60°C in order to inactivate endogenous AP. Bound AP-Nogo was detected by incubation with nitro blue tetrazolium. Note the intense neuronal staining by AP-Nogo that is displaced by unlabeled ligand. (c) is a graph displaying experimental data where the potency of AP-Nogo and GST-Nogo in E12 chick dorsal root ganglion growth cone collapse assays was assessed as described in the Example section. The EC<sub>50</sub> of AP-Nogo was determined to be 1 nM or less. The means  $\pm$  s.e.m. calculated from five to eight determinations are illustrated. (d) is a graph displaying experimental data where the binding of 10 nM AP-Nogo to chick E12 dorsal root ganglion neurons was assessed alone, or in the presence of 100 nM GST-Nogo or in the presence of 4  $\mu$ M Pep2, which was quantified from experiments as in (b) by the method described in the Example section. The means  $\pm$  s.e.m. calculated from eight determinations are shown. (e) is a graph displaying experimental data where AP-Nogo binding to dorsal root ganglion neurons was measured as a function of AP-Nogo concentration. This is one of six experiments with similar results. (f) is a graph summarizing the data from (e) replotted for Scatchard analysis. The apparent K<sub>d</sub> for AP-Nogo binding to E12 chick dorsal root ganglion neurons is 3 nM.



Figure 6 - Nogo binding to COS-7 expressing the Nogo receptor

This figure is a photograph of COS-7 cells that were transfected with an expression vector encoding the murine NgR. Two days after transfection, binding of AP-Nogo or AP was assessed as described in the Example section for dorsal root ganglion neurons. Note the selective binding of AP-Nogo to NgR expressing cells. Binding is greatly reduced in the presence of excess Nogo peptide not fused to AP.

Figure 7 - Structure of the Nogo receptor

This schematic diagram illustrates the major structural features of the NgR.

10

Figure 8 - Distribution of NgR mRNA.

This figure is a photograph of Northern blot of NgR mRNA for polyA<sup>+</sup> RNA samples from the indicated murine tissues on the left and for total RNA samples from various rat brain regions on the right. The migration of RNA size markers is shown at left.

15

Figure 9 - Nogo-66 Receptor Immunohistology

(a) is a photograph of an immunoblot where membrane fractions (10 µg protein) from the indicated cells or chick tissues were analyzed by anti-Nogo-66 receptor immunoblot (molecular weight markers in kDa are at right). (b) is a photograph of COS-7 cells expressing Myc-Nogo-66 receptor or chick E5 spinal cord explants (eight days *in vitro*) stained with anti-Nogo-66 receptor, anti-Myc or the oligodendrocyte-specific O4 antibody. The bottom three panels show double label immunohistochemistry of the same field (scale bar, 40 µm for the top three panels and 80 µm for the bottom three panels). (c) is a photograph of paraformaldehyde-fixed vibratome sections of adult brain or spinal cord stained with the anti-Nogo-66 receptor preparation. This demonstrates staining of axonal profiles (arrows) in both the pons and spinal cord. Staining is dramatically reduced in the presence of 10 µg/ml GST-Nogo-66 receptor antigen.

20

25

**Figure 10 - Nogo-66 Receptor mediates growth cone collapse by Nogo-66**

(a) is a photograph of chick E12 DRG explants exposed to Nogo-66 following pre-treatment with PI-PLC or buffer. Staining of F-actin in axons is illustrated (scale bar, 40  $\mu$ m). (b) is a graph summarizing the experimental results of binding of 3 nM AP or AP-Nogo to chick E12 dorsal root ganglion dissociated neurons. Where indicated the cultures were pre-treated with PI-PLC or 150 nM GST-Nogo-66 was included in the incubation with AP-Nogo. (c) is a graph summarizing growth cone collapse measurements from experiments as in (a). Chick E12 DRG cultures were treated with or without PI-PLC prior to exposure to 30 nM GST-Nogo-66 or 100 pM Sema3A. (d) is a photograph of E7 retinal ganglion cell explants infected with a control virus (HSV-PlexinA1) or with HSV-Myc-Nogo-66 receptor and then incubated with or without Nogo-66. Phalloidin staining of axonal growth cones is illustrated (scale bar, 25  $\mu$ m). (e) is a graph quantitating growth cone collapse in uninfected, or viral infected E7 retinal neurons as in (d).

15

**Figure 11 - Structure-function analysis of Nogo-66 receptor**

(a) is a schematic diagram of different Nogo-66 receptor deletion mutants. These mutants were assessed for level of expression by immunoblot and for AP-Nogo binding. Note that the leucine rich repeats and the leucine rich repeat carboxy terminal are required for Nogo binding but the remainder of the protein is not. The second protein was tested after purification and immobilization. (b) is a diagram of the predicted three dimensional structure for the first seven leucine rich repeats of the Nogo-66 receptor. This is derived from computer modeling based on the predicted structure of the related leucine rich repeats of the leutropin receptor (Jiang *et al.*, (1995) Structure 3, 1341-1353). Modeling is performed by Swiss-Model at [www.expasy.ch/spdbv](http://www.expasy.ch/spdbv). Those regions with beta sheet and alpha helix secondary structure are also indicated.

25

**Figure 12 - Soluble NgR blocks Nogo-66**

Chick E13 DRG neurons cultured under standard conditions. In growth cone collapse assays, conditioned medium from HEK 293T cells secreting the 1-348 amino acid ectodomain fragment of the murine NgR or control conditioned medium was added together with 100 nM Nogo-66. In the bottom left panel (b), the data in the graph demonstrates that Nogo-induced collapse is blocked by the soluble receptor fragment. (c) For outgrowth assays, neurons were cultured in the presence of control or NgR ectodomain conditioned medium together with Nogo-66 protein (50 nM) or central nervous system myelin (15  $\mu$ g total protein/ml). The top four panels (a) show photographs demonstrating that central nervous system myelin inhibits outgrowth and that this is blocked by the presence the NgR ectodomain protein. Outgrowth is quantitated in the graph in the bottom right panel.

**Figure 13 - Regions in the luminal/extracellular domain of Nogo necessary for NgR binding**

(a) graphically depicts the amino acid sequences of peptides derived from the luminal/extracellular domain of Nogo that were recombinantly attached to DNA encoding alkaline phosphatase (AP) and expressed to make AP fusion proteins. (b) shows the binding of the above AP fusion proteins to COS-7 cells expressing NgR. Conditioned medium from 293T cells expressing the AP fusion proteins or AP alone was applied to COS-7 cells transfected with mouse NgR (mNgR). Binding was visualized after application of substrates NBT and BCIP. Scale bar, 100 $\mu$ m.

**Figure 14 - Residues 1-40 of the luminal/extracellular domain of Nogo bind NgR**

(a) shows the binding of the fusion protein containing AP and the 1-40 peptide described in Figure 5a [hereinafter "140-AP"] to COS-7 cells expressing mouse NgR. Scale bar, 100 $\mu$ m. (b) graphically depicts the binding of 140-AP to COS-7 cells expressing mNgR as measured as a function of 140-AP concentration. (c) graphically depicts data derived from the above 140-AP binding assay replotted as bound/free v. bound. The K<sub>d</sub> of 140-AP binding to mNgR in this assay is 8nM.

**Figure 15 - Growth cone collapsing activity AP-fused peptides**

- (a) shows E12 chick DRG growth cone morphology following 30 minute exposure to 140-AP and AP-Nogo-66 fusion proteins. Scale bar, 25um. (b) graphically depicts the quantification of growth cone collapse in E12 chick DRG cultures after exposure to condition medium containing 20nM AP fusion proteins comprising AP fused to the following peptides as described in Figure 13a: 1-66, 1-40, 1-35 and 6-40. As a control, condition medium containing no AP fusion protein was used.

**Figure 16 - Peptide 140 neutralizes Nogo-66 inhibitory activity**

- (a) shows E12 chick DRG growth cone morphology after treatment with a synthetic peptide encoding amino acids # 1055-1094, acetylated at the C- terminus and amidated at the N-terminus of the human NogoA protein [hereinafter, "peptide 140"], the luminal/extracellular space encoded by SEQ ID NO:22. The cultures were pretreated with 1uM peptide 140 or buffer followed by a 30 minute exposure to 30nM GST-Nogo-66 or 12.5nM TPA. The amino acid sequence of peptide 140 corresponds to a sequence within the luminal/extracellular region of the hNogo protein. Scale bar 25um. Growth cones were visualized by rhodamine-phalloidin staining. (b)-(d) graphically depicts the amount of E12 chick DRG growth cone collapse after the cells have been pretreated with 1uM peptide 140, or buffer before a 30 minute exposure to various concentrations of GST-Nogo-66, TPA or Sema3A. (e) graphically depicts, as compared to a control, the percentage of neurite outgrowth in dissociated E12 chick DRG cultures grown for 5-7 hours in the presence of substrate coated with GST-Nogo-66 or phosphate buffered saline (PBS) following treatment with peptide 140, a scrambled version of peptide 140 (i.e., acetyl-SYVKEYAPIFAGKSRGEIKYQSIEIHEAQVRSDELVQSLN-amide) or buffer.

**Figure 17 - Peptide 140 partially blocks CNS myelin inhibitory activity**

(a) shows dissociated E12 chick DRG cultures grown on bound substrate coating (CNS myelin or PBS) following treatment with 1 $\mu$ M peptide 140, a scrambled version of peptide 140 or buffer. Scale bar 75 $\mu$ m. (b) graphically depicts the percentage of E12 chick DRG growth cone collapse in explant cultures pretreated with peptide 140 or buffer and then exposed to CNS myelin or PBS for 30 minutes before fixation. (c) graphically depicts the percentage of neurite outgrowth for E12 chick dissociated DRG neurite outgrowth grown for 5-7 hours on bound substrate coating (CNS myelin or PBS) following application of peptide 140, scrambled peptide 140 or buffer.

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**Figure 18. Nogo binding to NgR Deletion Mutants: LRRNT, LRR1-8 and LRRCT required for binding**

(A) WTNgR (wt) and the NgR deletion mutants used in this study are illustrated. NgR mutants include deletions to the amino terminus ( $\Delta$ NT), LRR domains 1 and 2 ( $\Delta$ 1-2), LRR domains 3 and 4 ( $\Delta$ 3-4), LRR domains 5 and 6 ( $\Delta$ 5-6), LRR domains 7 and 8 ( $\Delta$ 7-8), the LRR carboxy terminus ( $\Delta$ LRRCT), the NgR carboxy terminus ( $\Delta$ CT) and the complete LRR domain (LRR-). (B) COS-7 cells transfected with NgR deletion mutant plasmids were stained for anti-myc immunoreactivity or tested for AP-Nogo binding. All NgR mutant proteins were expressed in COS-7 cells as shown by myc immunoreactivity. Only wtNgR and NgRACT-transfected COS-7 cells bound to AP-Nogo. Scale bar, 100  $\mu$ m.

20

**Figure 19. Expression of HSVNgR proteins in retinal ganglion cell neurites**

(A) HSV plasmids encoding myc epitope-tagged wild-type NgR (mycNgR), L1NgR, and myc-tagged NgRACT were transfected into HEK293T cells and protein expression in cell lysates was analyzed by SDS-PAGE and immunoblotting with anti-myc and anti-NgR antibodies. All three proteins were expressed at the predicted molecular weight as demonstrated by anti-NgR immunoblotting. L1NgR encodes residues 1-451 of mouse NgR fused to the transmembrane and cytoplasmic tail of

25

mouse L1, but lacks a myc tag. (B) Anti-myc immunostaining of infected retinal explants demonstrates expression of mycNgR $\Delta$ CT in RGC neurites double stained with phalloidin. Myc-staining was negative in a phalloidin-stained neurite that was infected with HSVL1NgR.

5

Figure 20. NgRL1 mediates growth cone collapse in response to GST-hNogo-A(1055-1120) but NgR $\Delta$ CT does not

(A) E7 chick retinal explants were infected with recombinant viral preparations of PlexinA1 (PlexA1), wild-type NgR (wtNgR), NgRL1 chimeric receptor (NgRL1), or NgR carboxy terminal deletion mutant (NgR $\Delta$ CT). Explants were treated with GST-hNogo-A(1055-1120) for 30 min, and stained with rhodamine-phalloidin. Cells infected with PlexA1 virus or NgR $\Delta$ CT virus are insensitive to treatment with GST-hNogo-A(1055-1120), whereas wtNgR or NgRL1-infected cells collapse in response to GST-hNogo-A(1055-1120). (B) Dose curve of RGC response to varying amounts of GST-hNogo-A(1055-1120) following infection with NgR viral preparations.

Figure 21. GSTNgRCT does not constitutively inhibit neurite outgrowth

Neurite outgrowth of dissociated E13 DRGs plated on GST-hNogo-A(1055-1120) substrates in the presence of 100 nM GSTNgRCT or PBS as a control. GSTNgRCT does not inhibit neurite outgrowth on control PBS spots or modify the response of E13 DRGs to GST-hNogo-A(1055-1120) inhibition.

Figure 22. Analysis of NgR subcellular localization

Cell lysates from HEK293T cells transfected with HSVwtNgR or HSVNgRL1 plasmids were fractionated on OptiPrep flotation gradients. Fractions were separated by SDS-PAGE and analyzed by immunoblotting blots with anti-NgR, anti-TfR, or anti-caveolin antibodies. As predicted, wtNgR is found almost exclusively in the

caveolin-rich detergent insoluble fraction (A), whereas L1NgR is localized to multiple membrane fractions with a much smaller proportion in the caveolin-rich detergent insoluble fraction compared to wtNgR (B).

5    Figure 23. mNgR binds to mNgR

COS-7 cells were transfected with wtNgR or NgR deletion mutant plasmids and tested for AP-NgR binding. wtNgR and NgRΔCT- transfected COS-7 cells bind to AP-NgR whereas other NgR deletion mutants do not. Scale bar, 100 μm.

10   Figure 24. The soluble ectodomain of mNgR blocks inhibition of outgrowth by soluble hNogo-A(1055-1120) and CNS myelin

Chick E13 DRG neurons were cultured under standard conditions. In growth cone collapse assays, conditioned medium from HEK293T cells secreting the 1-348 as ectodomain fragment of the mNgR or control conditioned medium was added together  
15   with 100 nM GST-hNogo-A(1055-1120). In the bottom left panel, note that hNogo-A(1055-1120)-induced collapse is blocked by the soluble receptor fragment. For outgrowth assays, neurons were cultured in the presence of control or mNgR ectodomain conditioned medium together with GST-hNogo-A(1055-1120) protein (50 nM) or CNS myelin (15 μg total protein/ml). The top four panels show that CNS  
20   myelin inhibits outgrowth and that this is blocked by the presence the mNgR ectodomain protein.

## DETAILED DESCRIPTION OF THE INVENTION

### I. Definitions

25        Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention,

the preferred methods and materials are described.

As used herein, the term “axon” refers to a long cellular protrusion from a neuron, whereby efferent (outgoing) action potentials are conducted from the cell body towards target cells.

5       As used herein, the term “axonal growth” refers to an extension of the long process or axon, originating at the cell body and preceded by the growth cone.

As used herein, the term “central nervous system disease, disorder or injury” refers to any state associated with abnormal function of the central nervous system (CNS). The term includes, but is not limited to, altered CNS function resulting from  
10       physical trauma to cerebral or spinal chord tissue, viral infection, autoimmune mechanism, genetic mutation and neurodegenerative diseases or disorders.

As used herein, the term “chimeric protein” refers to any polypeptide which is not completely homologous at the amino acid level to its wild-type sequence or is encoded by a nucleic acid which is derived from splicing two distinct sources of  
15       nucleic acids. The term includes, but is not limited to, fusion proteins and proteins designed to contain one or more amino acid substitutions which distinguishes their amino acid sequence from the wild type sequence.

As used herein, the term “demyelinating disease” refers to a pathological disorder characterized by the degradation of the myelin sheath of the oligodendrocyte  
20       cell membrane.

As used herein, the term “neurite” refers to a process growing out of a neuron. As it is sometimes difficult to distinguish a dendrite from an axon in culture, the term neurite is used for both.

As used herein, the term “oligodendrocyte” refers to a neuroglial cell of the  
25       CNS whose function is to myelinate CNS axons.

As used herein, the term “polypeptide” refers to a peptide which on hydrolysis yields more than two amino acids, called tripeptides, tetrapeptides, etc. according to the number of amino acids contained in the polypeptide. The term “polypeptide” is



used synonymously with the term “protein” and “peptide” throughout the specification.

## II. Specific Embodiments

### 5 A. NgR Protein and Peptide Agents for the NgR Protein

The present invention provides isolated protein, allelic variants of the protein, and conservative amino acid substitutions of the protein. As used herein, the protein or polypeptide refers to a NgR protein that has the human amino acid sequence depicted in SEQ ID NO: 2 or the murine amino acid sequence depicted in SEQ ID  
10 NO: 4. The protein or polypeptide also refers to the peptides identified as NgR peptide agents that have the amino acid sequences depicted in SEQ ID NO: 8, 10, 12, 14, 16, 18 and 20. The invention also includes naturally occurring allelic variants and proteins that have a slightly different amino acid sequence than that specifically recited above. Allelic variants, though possessing a slightly different amino acid  
15 sequence than those recited above, will still have the same or similar biological functions associated with the human and murine NgR proteins and the NgR peptide agents depicted in SEQ ID NO: 2, 4, 8, 10, 12, 14, 16, 18 and 20.

As used herein, the family of proteins related to the NgR proteins refers to proteins that have been isolated from organisms in addition to humans and mice. The  
20 methods used to identify and isolate other members of the family of proteins related to the NgR proteins are described below.

The NgR proteins and peptide agents of the present invention are preferably in isolated form. As used herein, a protein or ligand is said to be isolated when physical, mechanical or chemical methods are employed to remove the protein from cellular  
25 constituents that are normally associated with the protein. A skilled artisan can readily employ standard purification methods to obtain an isolated protein or ligand.

The proteins of the present invention further include conservative variants of the proteins and ligands herein described. As used herein, a conservative variant refers to alterations in the amino acid sequence that do not adversely affect the

biological functions of the protein. A substitution, insertion or deletion is said to adversely affect the protein when the altered sequence prevents or disrupts a biological function associated with the protein. For example, the overall charge, structure or hydrophobic-hydrophilic properties of the protein can be altered without  
5 adversely affecting a biological activity. Accordingly, the amino acid sequence can be altered, for example to render the peptide more hydrophobic or hydrophilic, without adversely affecting the biological activities of the protein.

The allelic variants, the conservative substitution variants, and the members of the protein family, will have an amino acid sequence having at least seventy-five  
10 percent amino acid sequence identity with the human and murine sequences set forth in SEQ ID NO: 2, 4, 8, 10, 12, 14, 16, 18 and 20, more preferably at least eighty percent, even more preferably at least ninety percent, and most preferably at least ninety-five percent. Identity or homology with respect to such sequences is defined herein as the percentage of amino acid residues in the candidate sequence that are  
15 identical with the known peptides, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology, and not considering any conservative substitutions as part of the sequence identity. N-terminal, C-terminal or internal extensions, deletions, or insertions into the peptide sequence shall not be construed as affecting homology.

20 Thus, the proteins and peptides of the present invention include molecules comprising the amino acid sequence of SEQ ID NO: 2, 4, 8, 10, 12, 14, 16, 18 and 20; fragments thereof having a consecutive sequence of at least about 3, 4, 5, 6, 10, 15, 20, 25, 30, 35 or more amino acid residues of the NgR proteins and peptide agents; amino acid sequence variants of such sequences wherein at least one amino acid  
25 residue has been inserted N- or C-terminal to, or within, the disclosed sequence; amino acid sequence variants of the disclosed sequences, or their fragments as defined above, that have been substituted by another residue. Contemplated variants further include those containing predetermined mutations by, *e.g.*, homologous recombination, site-directed or PCR mutagenesis, and the corresponding proteins of

other animal species, including but not limited to rabbit, rat, porcine, bovine, ovine, equine and non-human primate species, the alleles or other naturally occurring variants of the family of proteins; and derivatives wherein the protein has been covalently modified by substitution, chemical, enzymatic, or other appropriate means  
5 with a moiety other than a naturally occurring amino acid (for example, a detectable moiety such as an enzyme or radioisotope).

As described below, members of the family of proteins can be used: (1) to identify agents which modulate at least one activity of the protein, (2) in methods of identifying binding partners for the protein, (3) as an antigen to raise polyclonal or  
10 monoclonal antibodies, and 4) as a therapeutic agent.

#### B. Nucleic Acid Molecules

The present invention further provides nucleic acid molecules that encode the proteins and peptides comprising the amino acid sequence of SEQ ID NO: 2, 4, 8, 10,  
15 12, 14, 16, 18 and 20 and the related proteins herein described, preferably in isolated form. As used herein, "nucleic acid" includes genomic DNA, cDNA, mRNA and antisense molecules, as well as nucleic acids based on alternative backbones or including alternative bases whether derived from natural sources or synthesized.

Homology or identity is determined by BLAST (Basic Local Alignment  
20 Search Tool) analysis using the algorithm employed by the programs blastp, blastn, blastx, tblastn and tblastx (Karlin *et al.*, (1990) Proc. Natl. Acad. Sci. USA 87, 2264-2268 and Altschul, (1993) J. Mol. Evol. 36, 290-300, fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments between a query sequence  
25 and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases see Altschul *et al.*, (1994) Nature Genetics 6, 119-129 which is fully incorporated by reference. The search parameters for

histogram, descriptions, alignments, expect (*i.e.*, the statistical significance threshold for reporting matches against database sequences), cutoff, matrix and filter are at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx is the BLOSUM62 matrix (Henikoff *et al.*, (1992) Proc. Natl. Acad. Sci. USA 89, 10915-10919, fully incorporated by reference). Four blastn parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every wink<sup>th</sup> position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent Blastp parameter settings were Q=9; R=2; wink=1; and gapw=32. A Bestfit comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

As used herein, "high stringency conditions" means hybridization at 42°C in the presence of 50% formamide, followed by a first wash at 65°C with 2× SSC containing 1% sodium SDS, followed by a second wash at 65°C with 0.1× SSC.

As used herein, a nucleic acid molecule is said to be "isolated" when the nucleic acid molecule is substantially separated from contaminant nucleic acid encoding other polypeptides from the source of nucleic acid.

The present invention further provides fragments of the encoding nucleic acid molecule. As used herein, a fragment of an encoding nucleic acid molecule refers to a portion of the entire protein encoding sequence. The size of the fragment will be determined by the intended use. For example, if the fragment is chosen so as to encode an active portion of the protein, the fragment will need to be large enough to encode the functional region(s) of the protein. If the fragment is to be used as a nucleic acid probe or PCR primer, then the fragment length is chosen so as to obtain a relatively small number of false positives during probing/priming.

Fragments of the encoding nucleic acid molecules of the present invention (*i.e.*, synthetic oligonucleotides) that are used as probes or specific primers for the polymerase chain reaction (PCR) or to synthesize gene sequences encoding proteins of the invention

can easily be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci *et al.*, (1981) J. Am. Chem. Soc. 103, 3185-3191 or using automated synthesis methods. In addition, larger DNA segments can readily be prepared by well known methods, such as synthesis of a group of oligonucleotides that define various modular segments of the gene, followed by ligation of oligonucleotides to build the complete modified gene.

The encoding nucleic acid molecules of the present invention may further be modified so as to contain a detectable label for diagnostic and probe purposes. A variety of such labels are known in the art and can readily be employed with the encoding molecules herein described. Suitable labels include, but are not limited to, biotin, radiolabeled nucleotides and the like. A skilled artisan can employ any of the art known labels to obtain a labeled encoding nucleic acid molecule.

Modifications to the primary structure by deletion, addition, or alteration of the amino acids incorporated into the protein sequence during translation can be made without destroying the activity of the protein. Such substitutions or other alterations result in proteins having an amino acid sequence encoded by a nucleic acid falling within the contemplated scope of the present invention.

The NgR domain designations used herein are defined as follows:

**Table 1. Example NgR domains**

Domain	hNgR (SEQ ID: 2)	mNgR (SEQ ID NO:4)
Signal Seq.	1-26	1-26
LRRNT	27-56	27-56
LRR1	57-81	57-81
LRR2	82-105	82-105
LRR3	106-130	106-130
LRR4	131-154	131-154
LRR5	155-178	155-178

	LRR6	179-202	179-202
	LRR7	203-226	203-226
	LRR8	227-250	227-250
	LRRCT	260-309	260-309
5	CTS (CT Signaling)	310-445	310-445
	GPI	446-473	456-473

In some embodiments of the invention, the above domains are modified.

Modification can be in a manner that preserves domain functionality. Modification can include addition, deletion, or substitution of certain amino acids. Exemplary  
10 modifications include conservative amino acid substitutions. Preferably such substitutions number 20 or fewer per 100 residues. More preferably, such substitutions number 10 or fewer per 100 residues. Further exemplary modifications include addition of flanking sequences of up to five amino acids at the N terminus and/or C terminus of one or more domains.

15 According to this invention, the signal sequence and GPI domains of the NgRs of this invention can be replaced by signal sequences and GPI domains of other proteins. In one embodiment of this invention, the signal sequence domain consists of #1-26 of the hNgR or #1-26 of the mNgR. The GPI domain function have been shown to anchor the proteins to lipid rafts (e.g., Tansey et al., Neuron 25:611-623 (2000)). GPI domains are  
20 known in the art, e.g., Gaudiz, et al., J. Biol. Chem. 273(40):26202-26209 (1998).

According to one embodiment of the invention, the GPI domain consists of #446-473 amino acid residues of hNgR or #456-473 amino acid residues of mNgR. Biologically active variants of the GPI domain include polypeptides comprising amino acid sequences that anchor proteins to lipid rafts.

25 The LRRNT domain is a leucine rich repeat domain that is typically flanking the N-terminal side of the LRR1-8 domain.

Leucine rich domains are also known in the art, e.g., Kobe, B. et al., TIBS 19(10):415-421 (1994). In one embodiment of this invention, the LRR1 domain, LRR2

domain, LRR3 domain, LRR4 domain, LRR5 domain, LRR6 domain, the LRR7 domain and the LRR8 domain (collectively, also known as LRR1-8 herein) consists of the amino acid residues as recited in Table 1. The The LR1-8 shares sequence identity with several other leucine rich proteins. According to one embodiment of this invention, a LRR  
5 domain of NgR is replaced with a LRR domain of another protein.

The LRRCT domain is a leucine rich repeat domain that is typically flanking the C-terminal side of the LRR1-8 domain.. According to one embodiment of the invention, the LRRCT domain consists of #-260-309 residues of hNgR or mNgR. According to one embodiment of the invention, the LRRCT domain consists of #-260-305 residues of hNgR  
10 or mNgR.

A polypeptide comprising a LRRNT domain, a LRR1-8 domain and a LRRCT domain (collectively, also referred to as a NTLRRCT domain (SEQ ID NO:55) herein) of NgR is contemplated. Biologically active variants of NTLRRCT include polypeptides comprising the NTLRRCT domain that can bind Nogo and/or can bind to NgR.

15 According,

A CTS domain is an amino acid sequence within a NgR between the LRRCT and the GPI domain. According to one embodiment, the CTS domain can be described by the residues recited above. A CTS domain according to this invention is involved in signalling a neuron in response to a Nogo ligand binding to the NgR. A “portion of a CTS  
20 domain” is 20 or more consecutive amino acids of a CTS domain. A portion of a CTS domain can also be selected from the group consisting of 30 or more, 40 or more, and 50 or more consecutive amino acids of a CTS domain. According to one embodiment of this invention, a NgR family member is manipulated so that the CTS region or a portion thereof is deleted, mutated or blocked with another agent so that it is not functional. In  
25 one embodiment, the CTS domain consists of #310-445 amino acid residue of hNgR or mNgR, or #306-442 of hNgR (SEQ ID NO:53). According to another embodiment, amino acid sequences that have a sequence identity to #310-445 amino acid residue of hNgR or mNgR, or #306-442 of hNgR in the range of 85% or more, 90% or more, 95% or more, 99% or more sequence identity are contemplated.

### C. Isolation of Other Related Nucleic Acid Molecules

As described above, the identification of the human nucleic acid molecule having SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17 and 19 allows a skilled artisan to isolate nucleic acid  
5 molecules that encode other members of the NgR protein family in addition to the sequences herein described. Further, the presently disclosed nucleic acid molecules allow a skilled artisan to isolate nucleic acid molecules that encode other members of the family of NgR proteins and peptide agents.

Essentially, a skilled artisan can readily use the amino acid sequence of SEQ ID  
10 NO: 2, 4, 8, 10, 12, 14, 16, 18 and 20 or an immunogenic fragment thereof to generate antibody probes to screen expression libraries prepared from appropriate cells. Typically, polyclonal antiserum from mammals such as rabbits immunized with the purified protein (as described below) or monoclonal antibodies can be used to probe a mammalian cDNA or genomic expression library, such as lambda gtl1 library, to obtain  
15 the appropriate coding sequence for other members of the protein family. The cloned cDNA sequence can be expressed as a fusion protein, expressed directly using its own control sequences, or expressed by constructions using control sequences appropriate to the particular host used for expression of the enzyme.

Alternatively, a portion of a coding sequence herein described can be synthesized  
20 and used as a probe to retrieve DNA encoding a member of the protein family from any mammalian organism. Oligomers containing *e.g.*, approximately 18-20 nucleotides (encoding about a six to seven amino acid stretch) can be prepared and used to screen genomic DNA or cDNA libraries to obtain hybridization under stringent conditions or conditions of sufficient stringency to eliminate an undue level of false positives.

25 Additionally, pairs of oligonucleotide primers can be prepared for use in a polymerase chain reaction (PCR) to selectively clone an encoding nucleic acid molecule. A PCR denature/anneal/extend cycle for using such PCR primers is well known in the art and can readily be adapted for use in isolating other encoding nucleic acid molecules.



D. Recombinant DNA Molecules Containing a Nucleic Acid Molecule

The present invention further provides recombinant DNA molecules (rDNA) that contain a coding sequence. As used herein, a rDNA molecule is a DNA molecule that has been subjected to molecular manipulation. Methods for generating rDNA molecules are well known in the art, for example, see Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press. In the preferred rDNA molecules, a coding DNA sequence is operably linked to expression control sequences and vector sequences.

The choice of vector and expression control sequences to which one of the protein family encoding sequences of the present invention is operably linked depends directly, as is well known in the art, on the functional properties desired (*e.g.*, protein expression, and the host cell to be transformed). A vector of the present invention may be at least capable of directing the replication or insertion into the host chromosome, and preferably also expression, of the structural gene included in the rDNA molecule.

Expression control elements that are used for regulating the expression of an operably linked protein encoding sequence are known in the art and include, but are not limited to, inducible promoters, constitutive promoters, secretion signals, and other regulatory elements. Preferably, the inducible promoter is readily controlled, such as being responsive to a nutrient in the host cell's medium.

In one embodiment, the vector containing a coding nucleic acid molecule will include a prokaryotic replicon, *i.e.*, a DNA sequence having the ability to direct autonomous replication and maintenance of the recombinant DNA molecule extra-chromosomally in a prokaryotic host cell, such as a bacterial host cell, transformed therewith. Such replicons are well known in the art. In addition, vectors that include a prokaryotic replicon may also include a gene whose expression confers a detectable marker such as a drug resistance. Typical of bacterial drug resistance genes are those that confer resistance to ampicillin or tetracycline.

Vectors that include a prokaryotic replicon can further include a prokaryotic or bacteriophage promoter capable of directing the expression (transcription and translation)

of the coding gene sequences in a bacterial host cell, such as *E. coli*. A promoter is an expression control element formed by a DNA sequence that permits binding of RNA polymerase and transcription to occur. Promoter sequences compatible with bacterial hosts are typically provided in plasmid vectors containing convenient restriction sites for  
5 insertion of a DNA segment of the present invention. Examples of such vector plasmids are pUC8, pUC9, pBR322 and pBR329 (Biorad Laboratories), pPL and pKK223 (Pharmacia). Any suitable prokaryotic host can be used to express a recombinant DNA molecule encoding a protein of the invention.

Expression vectors compatible with eukaryotic cells, preferably those  
10 compatible with vertebrate cells, can also be used to form a rDNA molecules that contains a coding sequence. Eukaryotic cell expression vectors are well known in the art and are available from several commercial sources. Typically, such vectors are provided containing convenient restriction sites for insertion of the desired DNA segment. Examples of such vectors are pSVL and pKSV-10 (Pharmacia), pBPV-1,  
15 pML2d (International Biotechnologies), pTDT1 (ATCC 31255) and the like eukaryotic expression vectors.

Eukaryotic cell expression vectors used to construct the rDNA molecules of the present invention may further include a selectable marker that is effective in an eukaryotic cell, preferably a drug resistance selection marker. A preferred drug  
20 resistance marker is the gene whose expression results in neomycin resistance, *i.e.*, the neomycin phosphotransferase (*neo*) gene. (Southern *et al.*, (1982) J. Mol. Anal. Genet. 1, 327-341). Alternatively, the selectable marker can be present on a separate plasmid, the two vectors introduced by co-transfection of the host cell, and transfectants selected by culturing in the appropriate drug for the selectable marker.

25

#### E. Host Cells Containing an Exogenously Supplied Coding Nucleic Acid Molecule

The present invention further provides host cells transformed with a nucleic acid molecule that encodes a protein of the present invention. The host cell can be either prokaryotic or eukaryotic. Eukaryotic cells useful for expression of a protein of

the invention are not limited, so long as the cell line is compatible with cell culture methods and compatible with the propagation of the expression vector and expression of the gene product. Preferred eukaryotic host cells include, but are not limited to, yeast, insect and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human cell line. Examples of useful eukaryotic host cells include Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells NIH-3T3 available from the ATCC as CRL1658, baby hamster kidney cells (BHK), and the like eukaryotic tissue culture cell lines.

Transformation of appropriate cell hosts with a rDNA molecule of the present invention is accomplished by well known methods that typically depend on the type of vector used and host system employed. With regard to transformation of prokaryotic host cells, electroporation and salt treatment methods can be employed (see, for example, Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press; Cohen *et al.*, (1972) Proc. Natl. Acad. Sci. USA 69, 2110-2114). With regard to transformation of vertebrate cells with vectors containing rDNA, electroporation, cationic lipid or salt treatment methods can be employed (see, for example, Graham *et al.*, (1973) Virology 52, 456-467; Wigler *et al.*, (1979) Proc. Natl. Acad. Sci. USA 76, 1373-1376).

Successfully transformed cells, *i.e.*, cells that contain a rDNA molecule of the present invention, can be identified by well known techniques including the selection for a selectable marker. For example, cells resulting from the introduction of an rDNA of the present invention can be cloned to produce single colonies. Cells from those colonies can be harvested, lysed and their DNA content examined for the presence of the rDNA using a method such as that described by Southern, (1975) J. Mol. Biol. 98, 503-517 or the proteins produced from the cell assayed via an immunological method.

#### F. Production of Recombinant Proteins using a rDNA Molecule

The present invention further provides methods for producing a protein of the

invention using nucleic acid molecules herein described. In general terms, the production of a recombinant form of a protein typically involves the following steps:

First, a nucleic acid molecule is obtained that encodes a protein of the invention, such as the nucleic acid molecule depicted in SEQ ID NO: 1, 3, 7, 9, 11,  
5 13, 15, 17 and 19 or nucleotides 166-1584 of SEQ ID NO: 1 and nucleotides 178-1596 of SEQ ID NO: 3. If the encoding sequence is uninterrupted by introns, it is directly suitable for expression in any host.

The nucleic acid molecule is then preferably placed in operable linkage with suitable control sequences, as described above, to form an expression unit containing  
10 the protein open reading frame. The expression unit is used to transform a suitable host and the transformed host is cultured under conditions that allow the production of the recombinant protein. Optionally the recombinant protein is isolated from the medium or from the cells; recovery and purification of the protein may not be necessary in some instances where some impurities may be tolerated.

Each of the foregoing steps can be done in a variety of ways. For example, the  
15 desired coding sequences may be obtained from genomic fragments and used directly in appropriate hosts. The construction of expression vectors that are operable in a variety of hosts is accomplished using appropriate replicons and control sequences, as set forth above. The control sequences, expression vectors, and transformation methods are  
20 dependent on the type of host cell used to express the gene and were discussed in detail earlier. Suitable restriction sites can, if not normally available, be added to the ends of the coding sequence so as to provide an excisable gene to insert into these vectors. A skilled artisan can readily adapt any host/expression system known in the art for use with the nucleic acid molecules of the invention to produce recombinant protein.

25

#### G. Methods to Identify Binding Partners

The present invention provides methods for use in isolating and identifying binding partners of proteins of the invention. In some embodiments, a protein of the invention is mixed with a potential binding partner or an extract or fraction of a cell under

conditions that allow the association of potential binding partners with the protein of the invention. After mixing, peptides, polypeptides, proteins or other molecules that have become associated with a protein of the invention are separated from the mixture. The binding partner bound to the protein of the invention can then be removed and further  
5 analyzed. To identify and isolate a binding partner, the entire protein, for instance the entire NgR protein of either SEQ ID NO: 2 or 4 or the entire Nogo protein of SEQ ID NO: 6 can be used. Alternatively, a fragment of the protein can be used.

As used herein, a cellular extract refers to a preparation or fraction which is made from a lysed or disrupted cell. The preferred source of cellular extracts will be cells  
10 derived from human brain or spinal cord tissue, for instance, human cerebral tissue. Alternatively, cellular extracts may be prepared from any source of neuronal tissue or available neuronal cell lines, particularly oligodendrocyte derived cell lines.

A variety of methods can be used to obtain an extract of a cell. Cells can be disrupted using either physical or chemical disruption methods. Examples of physical  
15 disruption methods include, but are not limited to, sonication and mechanical shearing. Examples of chemical lysis methods include, but are not limited to, detergent lysis and enzyme lysis. A skilled artisan can readily adapt methods for preparing cellular extracts in order to obtain extracts for use in the present methods.

Once an extract of a cell is prepared, the extract is mixed with the protein of the  
20 invention under conditions in which association of the protein with the binding partner can occur. A variety of conditions can be used, the most preferred being conditions that closely resemble conditions found in the cytoplasm of a human cell. Features such as osmolarity, pH, temperature, and the concentration of cellular extract used, can be varied to optimize the association of the protein with the binding partner.

25 After mixing under appropriate conditions, the bound complex is separated from the mixture. A variety of techniques can be utilized to separate the mixture. For example, antibodies specific to a protein of the invention can be used to immunoprecipitate the binding partner complex. Alternatively, standard chemical separation techniques such as chromatography and density-sediment centrifugation can be used.

After removal of non-associated cellular constituents found in the extract, the binding partner can be dissociated from the complex using conventional methods. For example, dissociation can be accomplished by altering the salt concentration or pH of the mixture.

5 To aid in separating associated binding partner pairs from the mixed extract, the protein of the invention can be immobilized on a solid support. For example, the protein can be attached to a nitrocellulose matrix or acrylic beads. Attachment of the protein to a solid support aids in separating peptide-binding partner pairs from other constituents found in the extract. The identified binding partners can be either a single protein or a  
10 complex made up of two or more proteins. Alternatively, binding partners may be identified using the Alkaline Phosphatase fusion assay according to the procedures of Flanagan & Vanderhaeghen, (1998) *Annu. Rev. Neurosci.* 21, 309-345 or Takahashi *et al.*, (1999) *Cell* 99, 59-69; the Far-Western assay according to the procedures of Takayama *et al.*, (1997) *Methods Mol. Biol.* 69, 171-184 or Sauder *et al.*, *J. Gen. Virol.*  
15 (1996) 77, 991-996 or identified through the use of epitope tagged proteins or GST fusion proteins.

Alternatively, the nucleic acid molecules of the invention can be used in a yeast two-hybrid system. The yeast two-hybrid system has been used to identify other protein partner pairs and can readily be adapted to employ the nucleic acid molecules herein  
20 described (see Stratagene Hybrizap® two-hybrid system).

#### H. Methods to Identify Agents that Modulate Activity

The present invention provides methods for identifying agents that modulate at least one activity of a NgR protein. The invention also provides methods for identifying  
25 agents that modulate at least one activity of a Nogo protein. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the specific activity of a NgR protein or Nogo protein, normalized to a standard unit, between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. Cell lines or

populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe.

Antibody probes can be prepared by immunizing suitable mammalian hosts  
5 utilizing appropriate immunization protocols using the NgR protein, Nogo protein, NgR peptide agents or immunogenic fragments of any of the foregoing. To enhance immunogenicity, these proteins or fragments can be conjugated to suitable carriers. Methods for preparing immunogenic conjugates with carriers such as BSA, KLH or other carrier proteins are well known in the art. In some circumstances, direct conjugation  
10 using, for example, carbodiimide reagents may be effective; in other instances linking reagents such as those supplied by Pierce Chemical Co. may be desirable to provide accessibility to the hapten. The hapten peptides can be extended at either the amino or carboxy terminus with a cysteine residue or interspersed with cysteine residues, for example, to facilitate linking to a carrier. Administration of the immunogens is conducted  
15 generally by injection over a suitable time period and with use of suitable adjuvants, as is generally understood in the art. During the immunization schedule, titers of antibodies are taken to determine adequacy of antibody formation.

While the polyclonal antisera produced in this way may be satisfactory for some applications, for pharmaceutical compositions, use of monoclonal preparations is  
20 preferred. Immortalized cell lines which secrete the desired monoclonal antibodies may be prepared using standard methods, see *e.g.*, Kohler & Milstein, (1992) *Biotechnology* 24, 524-526 or modifications which effect immortalization of lymphocytes or spleen cells, as is generally known. The immortalized cell lines secreting the desired antibodies can be screened by immunoassay in which the antigen is the peptide hapten, polypeptide or  
25 protein. When the appropriate immortalized cell culture secreting the desired antibody is identified, the cells can be cultured either *in vitro* or by production in ascites fluid.

The desired monoclonal antibodies may be recovered from the culture supernatant or from the ascites supernatant. The intact anti-Nogo or anti-NgR antibodies or fragments thereof can be used as *e.g.*, antagonists of binding between Nogo (ligand) and a NgR. Use

of immunologically reactive fragments, such as the Fab, Fab' of F(ab')<sub>2</sub> fragments is often preferable, especially in a therapeutic context, as these fragments are generally less immunogenic than the whole immunoglobulin.

The antibodies or fragments may also be produced, using current technology, by recombinant means. Antibody regions that bind specifically to the desired regions of the protein can also be produced in the context of chimeras with multiple species origin, for instance, humanized antibodies.

The antibody can therefore be a humanized antibody or human antibody, see, e.g., in U.S. Patent 5,585,089 or Riechmann *et al.*, (1988) Nature 332, 323-327.

Agents that are assayed in the above method can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a non-random basis which takes into account the sequence of the target site or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to the binding domain (SEQ ID NO: 20) of Nogo which interacts with the NgR. Alternatively, it can be a fragment of the binding domain, e.g., SEQ ID NO: 8, 10, 12, 14, 16 and 18.

The agents of the present invention can be, as examples, peptides, antibodies, antibody fragments, small molecules, vitamin derivatives, as well as carbohydrates. Peptide agents of the invention can be prepared using standard solid phase (or solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production



systems. The production using solid phase peptide synthesis is necessitated if non-gene-encoded amino acids are to be included.

Another class of agents of the present invention are antibodies or fragments thereof that bind to a Nogo protein or NgR protein. Antibody agents can be obtained by  
5 immunization of suitable mammalian subjects with peptides, containing as antigenic regions, those portions of the protein intended to be targeted by the antibodies.

#### I. High Throughput Assays

The power of high throughput screening is utilized to the search for new  
10 compounds which are capable of interacting with the NgR protein. For general information on high-throughput screening (e.g., Devlin, (1998) High Throughput Screening, Marcel Dekker; U.S. Patent 5,763,263). High throughput assays utilize one or more different assay techniques.

Immunodiagnosics and Immunoassays. These are a group of techniques used for  
15 the measurement of specific biochemical substances, commonly at low concentrations in complex mixtures such as biological fluids, that depend upon the specificity and high affinity shown by suitably prepared and selected antibodies for their complementary antigens. A substance to be measured must, of necessity, be antigenic -either an immunogenic macromolecule or a haptenic small molecule. To each sample a known,  
20 limited amount of specific antibody is added and the fraction of the antigen combining with it, often expressed as the bound:free ratio, is estimated, using as indicator a form of the antigen labeled with radioisotope (radioimmunoassay), fluorescent molecule (fluoroimmunoassay), stable free radical (spin immunoassay), enzyme (enzyme immunoassay), or other readily distinguishable label.

25 Antibodies can be labeled in various ways, including: enzyme-linked immunosorbent assay (ELISA); radioimmuno-assay (RIA); fluorescent immunoassay (FIA); chemiluminescent immunoassay (CLIA); and labeling the antibody with colloidal gold particles (immunoNogold).

Common assay formats include the sandwich assay, competitive or

competition assay, latex agglutination assay, homogeneous assay, microtitre plate format and the microparticle-based assay.

Enzyme-linked immunosorbent assay (ELISA). ELISA is an immunochemical technique that avoids the hazards of radiochemicals and the expense of fluorescence  
5 detection systems. Instead, the assay uses enzymes as indicators. ELISA is a form of quantitative immunoassay based on the use of antibodies (or antigens) that are linked to an insoluble carrier surface, which is then used to "capture" the relevant antigen (or antibody) in the test solution. The antigen-antibody complex is then detected by measuring the activity of an appropriate enzyme that had previously been covalently attached to the  
10 antigen (or antibody).

For information on ELISA techniques, see, for example, Crowther, (1995) ELISA - Theory and Practice (Methods in Molecular Biology), Humana Press; Challacombe & Kemeny, (1998) ELISA and Other Solid Phase Immunoassays - Theoretical and Practical Aspects, John Wiley; Kemeny, (1991) A Practical Guide to  
15 ELISA, Pergamon Press; Ishikawa, (1991) Ultrasensitive and Rapid Enzyme Immunoassay (Laboratory Techniques in Biochemistry and Molecular Biology) Elsevier.

Colorimetric Assays for Enzymes. Colorimetry is any method of quantitative chemical analysis in which the concentration or amount of a compound is determined by comparing the color produced by the reaction of a reagent with both standard and test  
20 amounts of the compound, *e.g.*, using a colorimeter or a spectrophotometer.

Standard colorimetric assays of beta-galactosidase enzymatic activity are well known to those skilled in the art (see, for example, Norton *et al.*, (1985) Mol. Cell. Biol. 5, 281-290). A colorimetric assay can be performed on whole cell lysates using O-nitrophenyl-beta-D-galactopyranoside (ONPG, Sigma) as the substrate in a standard  
25 colorimetric beta-galactosidase assay (Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press. Automated colorimetric assays are also available for the detection of beta-galactosidase activity (see *e.g.*, U.S. Patent 5,733,720).

Immunofluorescence Assays. Immunofluorescence or immunofluorescence

microscopy is a technique in which an antigen or antibody is made fluorescent by conjugation to a fluorescent dye and then allowed to react with the complementary antibody or antigen in a tissue section or smear. The location of the antigen or antibody can then be determined by observing the fluorescence by microscopy under ultraviolet  
5 light.

For general information on immunofluorescent techniques, see, for example, Knapp *et al.*, (1978) Immunofluorescence and Related Staining Techniques, Elsevier; Allan, (1999) Protein Localization by Fluorescent Microscopy - A Practical Approach (The Practical Approach Series) Oxford University Press; Caul, (1993)  
10 Immunofluorescence Antigen Detection Techniques in Diagnostic Microbiology, Cambridge University Press. For detailed explanations of immunofluorescent techniques applicable to the present invention, see U.S. Patent 5,912,176; U.S. Patent 5,869,264; U.S. Patent 5,866,319; and U.S. Patent 5,861,259.

15 J. Uses for Agents that Modulate Activity

As provided in the Examples, the Nogo and NgR proteins and nucleic acids, such as the proteins having the amino acid sequence of SEQ ID NO: 2, 4 or 6, are expressed in myelin derived from axon and dendrites. Agents that modulate or up- or down-regulate the expression of the Nogo or NgR protein or agents such as agonists or antagonists of at  
20 least one activity of the Nogo or NgR protein may be used to modulate biological and pathologic processes associated with the protein's function and activity. The invention is particularly useful in the treatment of human subjects.

Pathological processes refer to a category of biological processes which produce a deleterious effect. For example, expression of a protein of the invention may be  
25 associated with inhibition of axonal regeneration following cranial, cerebral or spinal trauma, stroke or a demyelinating disease. Such demyelinating diseases include, but are not limited to, multiple sclerosis, monophasic demyelination, encephalomyelitis, multifocal leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,

Alexander's disease, Canavan's disease, metachromatic leukodystrophy and Krabbe's disease. As used herein, an agent is said to modulate a pathological process when the agent reduces the degree or severity of the process. For instance, a demyelinating disease may be prevented or disease progression modulated by the administration of agents which  
5 reduce, promote or modulate in some way the expression or at least one activity of a protein of the invention.

In one example, administration of the Nogo peptide agents depicted in SEQ ID NO: 8, 10, 12, 14, 16, 18 and 20 can be used to treat a demyelinating disease associated with Nogo or the NgR protein. In another example, cells which express the peptide agents  
10 of the invention may be transplanted to a site spinal cord injury to facilitate axonal growth throughout the injured site. Such transplanted cells would provide a means for restoring spinal cord function following injury or trauma.

In yet another example, administration of soluble NgR protein that binds to Nogo can be used to treat a demyelinating disease associated with Nogo or the NgR protein.  
15 This agent can be used to prevent the binding of Nogo to cell bound NgR and act as an antagonist of Nogo. Soluble receptors have been used to bind cytokines or other ligands to regulate their function (Thomson, (1998) Cytokine Handbook, Academic Press). A soluble receptor occurs in solution, or outside of the membrane.

In other embodiments of the invention, the structure of the segment that associates  
20 with the membrane is modified (*e.g.*, DNA sequence polymorphism or mutation in the gene) so the receptor is not tethered to the membrane, or the receptor is inserted, but is not retained within the membrane. Thus, a soluble receptor, in contrast to the corresponding membrane bound form, differs in one or more segments of the gene or receptor protein that are important to its association with the membrane.

25 The agents of the present invention can be provided alone, or in combination, or in sequential combination with other agents that modulate a particular pathological process. For example, an agent of the present invention can be administered in combination with anti-inflammatory agents following stroke as a means for blocking further neuronal damage and inhibition of axonal regeneration. As used herein, two agents are said to be

administered in combination when the two agents are administered simultaneously or are administered independently in a fashion such that the agents will act at the same time.

The agents of the present invention can be administered via parenteral, subcutaneous, intravenous, intramuscular, intraperitoneal, transdermal, or buccal routes.

5 For example, an agent may be administered locally to a site of injury via microinfusion. Typical sites include, but are not limited to, damaged areas of the spinal cord resulting from injury or damaged sites in the brain resulting from a stroke. Alternatively, or concurrently, administration may be by the oral route. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment,

10 if any, frequency of treatment, and the nature of the effect desired.

The present invention further provides compositions containing one or more agents which modulate expression or at least one activity of a protein of the invention. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art. Typical dosages comprise 1 pg/kg to 100 mg/kg

15 body weight. The preferred dosages for systemic administration comprise 100 ng/kg to 100 mg/kg body weight. The preferred dosages for direct administration to a site via microinfusion comprise 1 ng/kg to 1 µg/kg body weight.

In addition to the pharmacologically active agent, the compositions of the present invention may contain suitable pharmaceutically acceptable carriers comprising excipients

20 and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically for delivery to the site of action. Suitable formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be

25 administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol and dextran. Optionally, the suspension may also contain stabilizers. Liposomes can also be used to

encapsulate the agent for delivery into the cell.

The pharmaceutical formulation for systemic administration according to the invention may be formulated for enteral, parenteral or topical administration. Indeed, all three types of formulations may be used simultaneously to achieve systemic  
5 administration of the active ingredient. Suitable formulations for oral administration include hard or soft gelatin capsules, pills, tablets, including coated tablets, elixirs, suspensions, syrups or inhalations and controlled release forms thereof.

In practicing the methods of this invention, the agents of this invention may be used alone or in combination, or in combination with other therapeutic or diagnostic  
10 agents. In certain preferred embodiments, the compounds of this invention may be co-administered along with other compounds typically prescribed for these conditions according to generally accepted medical practice, such as anti-inflammatory agents, anticoagulants, antithrombotics, including platelet aggregation inhibitors, tissue plasminogen activators, urokinase, prourokinase, streptokinase, aspirin and heparin. The  
15 compounds of this invention can be utilized *in vivo*, ordinarily in mammals, such as humans, sheep, horses, cattle, pigs, dogs, cats, rats and mice, or *in vitro*.

#### K. Peptide Mimetics.

This invention also includes peptide mimetics which mimic the three-dimensional  
20 structure of Nogo and block Nogo binding at the NgR. Such peptide mimetics may have significant advantages over naturally-occurring peptides, including, for example: more economical production, greater chemical stability, enhanced pharmacological properties (half-life, absorption, potency, efficacy, etc.), altered specificity (*e.g.*, a broad-spectrum of biological activities), reduced antigenicity, and others.

25 In one form, mimetics are peptide-containing molecules that mimic elements of protein secondary structure. (see, for example, Johnson *et al.*, (1993) Peptide Turn Mimetics, in Biotechnology and Pharmacy, Pezzuto *et al.*, (editors) Chapman and Hall). The underlying rationale behind the use of peptide mimetics is that the peptide backbone of proteins exists chiefly to orient amino acid side chains in such a way as to facilitate

molecular interactions, such as those of antibody and antigen. A peptide mimetic is expected to permit molecular interactions similar to the natural molecule.

In another form, peptide analogs are commonly used in the pharmaceutical industry as non-peptide drugs with properties analogous to those of the template peptide.

- 5 These types of non-peptide compounds are also referred to as "peptide mimetics" or "peptidomimetics" (Fauchere, (1986) *Adv. Drug Res.* 15, 29-69; Veber & Freidinger, (1985) *Trends Neurosci.* 8, 392-396; Evans *et al.*, (1987) *J. Med. Chem.* 30, 1229-1239, which are incorporated herein by reference) and are usually developed with the aid of computerized molecular modeling.
- 10 Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce an equivalent therapeutic or prophylactic effect. Generally, peptide mimetics are structurally similar to a paradigm polypeptide (*i.e.*, a polypeptide that has a biochemical property or pharmacological activity), such as the extracellular domain of Nogo, but have one or more peptide linkages optionally replaced by a linkage selected
- 15 from the group consisting of: -CH<sub>2</sub>NH-, -CH<sub>2</sub>S-, -CH<sub>2</sub>-CH<sub>2</sub>-, -CH=CH- (cis and trans), -COCH<sub>2</sub>-, -CH(OH)CH<sub>2</sub>- and -CH<sub>2</sub>SO-, by methods known in the art and further described in the following references; Weinstein, (1983) *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Marcel Dekker; Morley, (1980) *Trends Pharmacol. Sci.* 1, 463-468 (general review); Hudson *et al.*, (1979) *Int. J. Pept. Protein Res.* 14, 177-185 (-CH<sub>2</sub>NH-, CH<sub>2</sub>CH<sub>2</sub>-); Spatola *et al.*, (1986) *Life Sci.* 38, 1243-1249 (-CH<sub>2</sub>-S); Hann, (1982) *J. Chem. Soc. Perkin Trans. 1*, 307-314 (-CH-CH-, cis and trans); Almquist *et al.*, (1980) *J. Med. Chem.* 23, 1392-1398 (-COCH<sub>2</sub>-); Jennings-White *et al.*, (1982) *Tetrahedron Lett.* 23, 2533 (-COCH<sub>2</sub>-); Holladay *et al.*, (1983) *Tetrahedron Lett.* 24, 4401-4404 (-C(OH)CH<sub>2</sub>-); and Hruby, (1982) *Life Sci.* 31, 189-199 (-CH<sub>2</sub>S-); each of
- 25 which is incorporated herein by reference.

Labeling of peptide mimetics usually involves covalent attachment of one or more labels, directly or through a spacer (*e.g.*, an amide group), to non-interfering position(s) on the peptide mimetic that are predicted by quantitative structure-activity data and molecular modeling. Such non-interfering positions generally are positions that do not form direct

contacts with the macromolecule(s) (e.g., are not contact points in Nogo-NgR complexes) to which the peptide mimetic binds to produce the therapeutic effect. Derivatization (e.g., labeling) of peptide mimetics should not substantially interfere with the desired biological or pharmacological activity of the peptide mimetic.

- 5           Nogo peptide mimetics can be constructed by structure-based drug design through replacement of amino acids by organic moieties (see, for example, Hughes, (1980) *Philos. Trans. R. Soc. Lond.* 290, 387-394; Hodgson, (1991) *Biotechnol.* 9, 19-21; Suckling, (1991) *Sci. Prog.* 75, 323-359).

- The use of peptide mimetics can be enhanced through the use of combinatorial  
10   chemistry to create drug libraries. The design of peptide mimetics can be aided by identifying amino acid mutations that increase or decrease binding of Nogo at the NgR. Approaches that can be used include the yeast two hybrid method (see Chien *et al.*, (1991) *Proc. Natl. Acad. Sci. USA* 88, 9578-9582) and using the phage display method. The two hybrid method detects protein-protein interactions in yeast (Fields *et al.*, (1989) *Nature*  
15   340, 245-246). The phage display method detects the interaction between an immobilized protein and a protein that is expressed on the surface of phages such as lambda and M13 (Amberg *et al.*, (1993) *Strategies* 6, 2-4; Hogrefe *et al.*, (1993) *Gene* 128, 119-126). These methods allow positive and negative selection for protein-protein interactions and the identification of the sequences that determine these interactions.

- 20           For general information on peptide synthesis and peptide mimetics, see, for example; Jones, (1992) *Amino Acid and Peptide Synthesis*, Oxford University Press; Jung, (1997) *Combinatorial Peptide and Nonpeptide Libraries: A Handbook*, John Wiley; Bodanszky *et al.*, (1993) *Peptide Chemistry - A Practical Textbook*, Springer Verlag.

25   L. Transgenic Animals

          The term "animal" as used herein includes all vertebrate animals, except humans. It also includes an individual animal in all stages of development, including embryonic and fetal stages. A "transgenic animal" is an animal containing one or more cells bearing genetic information received, directly or indirectly, by deliberate genetic manipulation at a



subcellular level, such as by microinjection or infection with recombinant virus. This introduced DNA molecule may be integrated within a chromosome, or it may be extra-chromosomally replicating DNA. The term "germ cell-line transgenic animal" refers to a transgenic animal in which the genetic information was introduced into a germ  
5 line cell, thereby conferring the ability to transfer the information to offspring. If such offspring in fact possess some or all of that information, then they, too, are transgenic animals. Transgenic animals containing mutant, knock-out, modified genes or gene constructs to over-express or conditionally express a polypeptide encoded by the cDNA sequences of SEQ ID NO: 1 or 3 or related sequences are encompassed in the invention.

10 To be expressed, a coding sequence should be operably linked to a regulatory region. Regulatory regions, such as promoters, may be used to increase, decrease, regulate or designate to certain tissues or to certain stages of development the expression of a gene. The promoter need not be a naturally occurring promoter. The "transgenic non-human animals" of the invention are produced by introducing "transgenes" into the germline of  
15 the non-human animal. The methods enabling the introduction of DNA into cells are generally available and well-known in the art. Different methods of introducing transgenes could be used. Generally, the zygote is the best target for microinjection. In the mouse, the male pronucleus reaches the size of approximately twenty microns in diameter, which allows reproducible injection of one to two picoliters of DNA solution.  
20 The use of zygotes as a target for gene transfer has a major advantage. In most cases, the injected DNA will be incorporated into the host genome before the first cleavage (Brinster *et al.*, (1985) Proc. Natl. Acad. Sci. USA 82, 4438-4442). Consequently, nearly all cells of the transgenic non-human animal will carry the incorporated transgene. Generally, this will also result in the efficient transmission of the transgene to offspring of the founder  
25 since 50% of the germ cells will harbor the transgene. Microinjection of zygotes is a preferred method for incorporating transgenes in practicing the invention.

Retroviral infection can also be used to introduce a transgene into a non-human animal. The developing non-human embryo can be cultured *in vitro* to the blastocyst stage. During this time, blastomeres may be targets for retroviral infection. Efficient

infection of the blastomeres is obtained by enzymatic treatment to remove the zona pellucida. The viral vector system used to introduce the transgene is typically a replication-defective retrovirus carrying the transgene (Jahner *et al.*, (1985) Proc. Natl. Acad. Sci. USA 82, 6927-6931; Van der Putten *et al.*, (1985) Proc. Natl. Acad. Sci. USA 82, 6148-6152). Transfection is easily and efficiently obtained by culturing the blastomeres on a monolayer of virus-producing cells (Van der Putten *et al.*, (1985) Proc. Natl. Acad. Sci. USA 82, 6148-6152; Stewart *et al.*, (1987) EMBO J. 6, 383-388). Alternatively, infection can be performed at a later stage. Virus or virus-producing cells can be injected into the blastocoele (Jahner *et al.*, (1982) Nature 298, 623-628). Most of the founder animals will be mosaic for the transgene since incorporation occurs only in a subset of the cells which formed the transgenic non-human animal. Furthermore, the founder animal may contain retroviral insertions of the transgene at a variety of positions in the genome; these generally segregate in the offspring. In addition, it is also possible to introduce transgenes into the germ line, albeit with low efficiency, by intrauterine retroviral infection of the midgestation embryo (Jahner *et al.*, (1982) Nature 298, 623-628).

A third type of target cell for transgene introduction is the embryonal stem cell (ES). ES cells are obtained from pre-implantation embryos cultured *in vitro* (Evans *et al.*, (1981) Nature 292, 154-156; Bradley *et al.*, (1984) Nature 309, 255-256; Gossler *et al.*, (1986) Proc. Natl. Acad. Sci. USA 83, 9065-9069). Transgenes can be efficiently introduced into ES cells by DNA transfection or by retrovirus-mediated transduction. The resulting transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The ES cells colonize the embryo and contribute to the germ line of the resulting chimeric animal.

The methods for evaluating the presence of the introduced DNA as well as its expression are readily available and well-known in the art. Such methods include, but are not limited to DNA (Southern) hybridization to detect the exogenous DNA, polymerase chain reaction (PCR), polyacrylamide gel electrophoresis (PAGE) and Western blots to detect DNA, RNA and protein. The methods include immunological and histochemical

techniques to detect expression of a NgR gene.

As discussed above, a nucleic acid of the invention can be transfected into a host cell using a vector. Preferred vectors are plasmids and viral vectors, such as retroviruses. Viral vectors may be used to produce a transgenic animal according to the invention.

5 Preferably, the viral vectors are replication defective, that is, they are unable to replicate autonomously in the target cell. In general, the genome of the replication defective viral vectors which are used within the scope of the present invention lack at least one region which is necessary for the replication of the virus in the infected cell. These regions can either be eliminated (in whole or in part), or be rendered non-functional by any technique  
10 known to a person skilled in the art. These techniques include the total removal, substitution (by other sequences, in particular by the inserted nucleic acid), partial deletion or addition of one or more bases to an essential (for replication) region. Such techniques may be performed *in vitro* (on the isolated DNA) or *in situ*, using the techniques of genetic manipulation or by treatment with mutagenic agents.

15 Preferably, the replication defective virus retains the sequences of its genome which are necessary for encapsidating the viral particles. The retroviruses are integrating viruses which infect dividing cells. The retrovirus genome includes two LTRs, an encapsidation sequence and three coding regions (*gag*, *pol* and *env*). The construction of recombinant retroviral vectors has been described (see, for example, Bernstein *et al.*,  
20 (1985) Genet. Eng. 7, 235; McCormick, (1985) Biotechnol. 3, 689-691). In recombinant retroviral vectors, the *gag*, *pol* and *env* genes are generally deleted, in whole or in part, and replaced with a heterologous nucleotide sequence of interest. These vectors can be constructed from different types of retrovirus, such as, HIV, MoMuLV (murine Moloney leukemia virus), MSV (murine Moloney sarcoma virus), HaSV (Harvey sarcoma virus);  
25 SNV (spleen necrosis virus); RSV (Rous sarcoma virus) and Friend virus.

In general, in order to construct recombinant retroviruses containing a nucleotide sequence, a plasmid is constructed which contains the LTRs, the encapsidation sequence and the coding sequence. This construct is used to transfect a packaging cell line, which cell line is able to supply in trans the retroviral functions which are deficient in the

plasmid. In general, the packaging cell lines are thus able to express the *gag*, *pol* and *env* genes. Such packaging cell lines have been described in the prior art, in particular the cell line PA317 (U.S. Patent 4,861,719); the PsiCRIP cell line (WO9002806) and the GP+envAm-12 cell line (WO8907150). In addition, the recombinant retroviral vectors

5 can contain modifications within the LTRs for suppressing transcriptional activity as well as extensive encapsidation sequences which may include a part of the *gag* gene (Bender *et al.*, (1987) J. Virol. 61, 1639-1646). Recombinant retroviral vectors are purified by standard techniques known to those having ordinary skill in the art.

In one aspect the nucleic acid encodes antisense RNA molecules. In this

10 embodiment, the nucleic acid is operably linked to suitable regulatory regions (discussed above) enabling expression of the nucleotide sequence, and is introduced into a cell utilizing, preferably, recombinant vector constructs, which will express the antisense nucleic acid once the vector is introduced into the cell. Examples of suitable vectors includes plasmids, adenoviruses, adeno-associated viruses (see, for example, U.S. Patent

15 4,797,368, U.S. Patent 5,139,941), retroviruses (see above), and herpes viruses. For delivery of a therapeutic gene the vector is preferably an adeno-associated virus.

Adenoviruses are eukaryotic DNA viruses that can be modified to efficiently deliver a nucleic acid of the invention to a variety of cell types. Various serotypes of adenovirus exist. Of these serotypes, preference is given, within the scope of the present

20 invention, to using type two or type five human adenoviruses (Ad 2 or Ad 5) or adenoviruses of animal origin (see WO9426914). Those adenoviruses of animal origin which can be used within the scope of the present invention include adenoviruses of canine, bovine, murine, ovine, porcine, avian, and simian origin.

The replication defective recombinant adenoviruses according to the invention can

25 be prepared by any technique known to the person skilled in the art. In particular, they can be prepared by homologous recombination between an adenovirus and a plasmid which carries, inter alia, the DNA sequence of interest. The homologous recombination is effected following cotransfection of the said adenovirus and plasmid into an appropriate cell line. The cell line which is employed should preferably (i) be transformable by the

said elements, and (ii) contain the sequences which are able to complement the part of the genome of the replication defective adenovirus, preferably in integrated form in order to avoid the risks of recombination. Recombinant adenoviruses are recovered and purified using standard molecular biological techniques, which are well known to one of ordinary skill in the art.

A number of recombinant or transgenic mice have been produced, including those which express an activated oncogene sequence (U.S. Patent 4,736,866); express Simian SV 40 T-antigen (U.S. Patent 5,728,915); lack the expression of interferon regulatory factor 1 (IRF-1) (U.S. Patent 5,731,490); exhibit dopaminergic dysfunction (U.S. Patent 5,723,719); express at least one human gene which participates in blood pressure control (U.S. Patent 5,731,489); display greater similarity to the conditions existing in naturally occurring Alzheimer's disease (U.S. Patent 5,720,936); have a reduced capacity to mediate cellular adhesion (U.S. Patent 5,602,307); possess a bovine growth hormone gene (Clutter *et al.*, (1996) Genetics 143, 1753-1760) or are capable of generating a fully human antibody response (Zou *et al.*, (1993) Science 262, 1271-1274).

While mice and rats remain the animals of choice for most transgenic experimentation, in some instances it is preferable or even necessary to use alternative animal species. Transgenic procedures have been successfully utilized in a variety of non-murine animals, including sheep, goats, chickens, hamsters, rabbits, cows and guinea pigs (see Aigner *et al.*, (1999) Biochem. Biophys. Res. Commun. 257, 843-850; Castro *et al.*, (1999) Genet. Anal. 15, 179-187; Brink *et al.*, (2000) Theriogenology 53, 139-148; Colman, (1999) Genet. Anal. 15, 167-173; Eyestone, (1999) Theriogenology 51, 509-517; Baguisi *et al.*, (1999) Nat. Biotechnol. 17, 456-461; Prather *et al.*, (1999) Theriogenology 51, 487-498; Pain *et al.*, (1999) Cells Tissues Organs 165, 212-219; Fernandez *et al.*, (1999) Indian J. Exp. Biol. 37, 1085-1092; U.S. Patent 5,908,969; U.S. Patent 5,792,902; U.S. Patent 5,892,070; U.S. Patent 6,025,540).

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following

working examples therefore, specifically point out preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

#### 5 Key for Sequence Listing

	<b>SEQ ID NO:</b>	<b>Description</b>
	SEQ ID NO:1	human NgR nucleotide sequence
	SEQ ID NO:2	human NgR amino acid sequence
	SEQ ID NO:3	mouse NgR nucleotide sequence
10	SEQ ID NO:4	mouse NgR amino acid sequence
	SEQ ID NO:5	human NogoA nucleotide sequence
	SEQ ID NO:6	human NogoA amino acid sequence
	SEQ ID NO:7	a nucleotide sequence coding for amino acid residues #1054-1078 of a human NogoA
15	SEQ ID NO:8	amino acid residues #1064-1088 of human NogoA
	SEQ ID NO:9	a nucleotide sequence coding for amino acid residues #1064-1088 of a human NogoA
	SEQ ID NO:10	amino acid residues #1064-1088 of human NogoA
20	SEQ ID NO:11	a nucleotide sequence coding for amino acid residues #1064-1088 of a human NogoA
	SEQ ID NO:12	amino acid residues #1064-1088 of a human NogoA
	SEQ ID NO:13	a nucleotide sequence coding for amino acid residues #1084-1108 of a human NogoA
25	SEQ ID NO:14	amino acid residues #1084-1108 of a human NogoA

5	SEQ ID NO:15	a nucleotide sequence coding for amino acid residues #1095-1119 of a human NogoA
	SEQ ID NO:16	amino acid residues #1095-1119 of a human NogoA
	SEQ ID NO:17	a nucleotide sequence coding for amino acid residues #1055-1094 of a human NogoA
	SEQ ID NO:18	amino acid residues #1055-1094 of a human NogoA
	SEQ ID NO:19	a nucleotide sequence coding for amino acid residues #1054-1119 of a human NogoA
10	SEQ ID NO:20	amino acid residues #1054-1119 of a human NogoA
	SEQ ID NO:21	a nucleotide sequence coding for amino acid residues #1055-1120 of a human NogoA
	SEQ ID NO:22	amino acid residues #1055-1120 of a human NogoA
	SEQ ID NO:23	a nucleotide sequence coding for amino acid residues #1055-1079 of a human NogoA
	SEQ ID NO:24	amino acid residues #1055-1079 of a human NogoA
15	SEQ ID NO:25	a nucleotide sequence coding for amino acid residues #1055-1084 of a human NogoA
	SEQ ID NO:26	amino acid residues #1055-1084 of a human NogoA
	SEQ ID NO:27	a nucleotide sequence coding for amino acid residues #1055-1089 of a human NogoA
	SEQ ID NO:28	amino acid residues #1055-1089 of a human NogoA
	SEQ ID NO:29	a nucleotide sequence coding for amino acid residues #1060-1094 of a human NogoA
20	SEQ ID NO:30	amino acid residues #1060-1094 of a human NogoA

	SEQ ID NO:31	a nucleotide sequence coding for amino acid residues #1065-1094 of a human NogoA
	SEQ ID NO:32	amino acid residues #1065-1094 of a human NogoA
	SEQ ID NO:33	a nucleotide sequence coding for amino acid residues #1070-1084 of a human NogoA
5	SEQ ID NO:34	amino acid residues #1070-1084 of a human NogoA
	SEQ ID NO:35	a nucleotide sequence coding for amino acid residues #1085-1109 of a human NogoA
	SEQ ID NO:36	amino acid residues #1085-1109 of a human NogoA
	SEQ ID NO:37	$\Delta$ LRR-NT5' primer
10	SEQ ID NO:38	NgR3X primer
	SEQ ID NO:39	MycNgR305 primer
	SEQ ID NO:40	MycNgR primer
	SEQ ID NO:41	2NgRt313 primer
	SEQ ID NO:42	TM/GPI5' primer
15	SEQ ID NO:43	DEL LRR1 primer
	SEQ ID NO:44	DEL LRR2 primer
	SEQ ID NO:45	DEL LRR3 primer
	SEQ ID NO:46	DEL LRR4 primer
	SEQ ID NO:47	DEL LRR5 primer
20	SEQ ID NO:48	DEL LRR6 primer
	SEQ ID NO:49	DEL LRR7 primer
	SEQ ID NO:50	DEL LRR8 primer
	SEQ ID NO:51	3DLRR CT primer
	SEQ ID NO:52	5 DLRRCT primer
25	SEQ ID NO:53	amino acid residues #306-442 of a human NgR



SEQ ID NO:54	amino acid residues #306-473 of a human NgR
SEQ ID NO:55	amino acid residues #27-309 of a human NgR

## EXAMPLES

### 5 Example 1 - Identification of Nogo as a Member of the Reticulon Family of Proteins

Adult mammalian axon regeneration is generally successful in the periphery but  
dismally poor in the CNS. However, many classes of CNS axons can extend for long  
distances in peripheral nerve grafts (Benfy & Aguayo (1982) *Nature* 296, 150-152).  
Comparison of CNS and peripheral nervous system (PNS) myelin has revealed that CNS  
10 white matter is selectively inhibitory for axonal outgrowth (Schwab & Thoenen (1985) *J.*  
*Neurosci.* 5, 2415-2423). Several components of CNS white matter, NI35, NI250 (Nogo)  
and MAG, with inhibitory activity for axon extension have been described (Wang *et al.*,  
(1999) *Transduction of inhibitory signals by the axonal growth cone, in Neurobiology of*  
*Spinal Cord Injury*, Kalb & Strittmatter (editors) Humana Press; Caroni & Schwab, (1988)  
15 *J. Cell Biol.* 106, 1281-1288; Spillmann *et al.*, (1998) *J. Biol. Chem.* 73, 19283-19293;  
McKerracher *et al.*, (1994) *Neuron* 13, 805-811; Mukhopadhyay *et al.*, (1994) *Neuron* 13,  
757-767.) The IN-1 antibody raised against NI35 and NI250 (Nogo) has been reported to  
allow moderate degrees of axonal regeneration and functional recovery after spinal cord  
injury (Bregman *et al.*, (1995) *Nature* 378, 498-501; Thallmair *et al.*, (1998) *Nature*  
20 *Neurosci.* 1, 24-31). The present invention identifies Nogo as a member of the Reticulon  
protein family.

Nogo is expressed by oligodendrocytes but not by Schwann cells, and associates  
primarily with the endoplasmic reticulum. The 66 amino acid lumenal-extracellular  
domain of Nogo (SEQ ID NO: 20) inhibits axonal extension and collapses dorsal root  
25 ganglion growth cones. Other Reticulon proteins are not expressed by oligodendrocytes,  
and the 66 amino acid lumenal-extracellular domain from other Reticulon proteins does  
not inhibit axonal regeneration. These data provide a molecular basis to assess the  
contribution of Nogo to the failure of axonal regeneration in the adult CNS.

For expression and protein purification of recombinant Nogo-A, the full length sequence (KIAA0886) was generously provided by the Kazusa DNA Research Institute. The full length coding sequence was amplified by the polymerase chain reaction (PCR) and ligated into the pCDNA3.1-MycHis vector (Invitrogen) to generate a plasmid  
5 encoding Nogo-A fused at the carboxyl terminus to the Myc epitope (Nogo-A-Myc). Alternatively, the coding sequence was amplified using primers that encode an in-frame Myc epitope immediately amino terminal to the first residue and a stop codon at the carboxyl terminus (Myc-Nogo-A). The Nogo-C-MycHis and Rtn1C-MycHis expression vectors were derived in the same fashion except that an adult rat brain cDNA library was  
10 used as template for a PCR reaction with primers was based on the Nogo-C or Rtn1C sequences (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416). These plasmids were transfected into COS-7 or HEK293T by the Lipofectamine (Gibco-BRL) or the FuGENE 6 (Boehringer Mannheim) method.

A portion of Nogo-A encoding the 66 amino acid lumenal-extracellular fragment  
15 of Nogo-A was amplified by PCR and ligated into the pGEX-2T plasmid to yield a prokaryotic expression vector for the GST-Nogo fusion protein. Similar regions of Rtn1, Rtn2 and Rtn3 were amplified by nested PCR using an adult rat brain cDNA library as template and ligated to pGEX-2T. *E. coli* transformed with these plasmids were induced with IPTG. Soluble, native GST fusion proteins were purified using a glutathione-resin  
20 and contained approximately 75% GST and 25% full length GST-Nogo or GST-Rtn protein. The majority of the GST-Nogo protein was not extractable from under non-denaturing conditions, but an 8 M urea extract dialyzed against PBS contained over 98% pure GST-Nogo.

Myc immunoreactivity is detectable with an apparent size in the 225 kDa range  
25 under reducing conditions (data not shown). Thus, the cDNA directs the expression of a protein with appropriate electrophoretic mobility and the amino acid sequence to be Nogo which was termed human Nogo-A (hNogo-A).

The conserved carboxyl tail of the Rtn family proteins contains two hydrophobic domains separated by a 66 amino acid residue hydrophilic segment. None of the

sequences contain a signal peptide. The predicted topology for these proteins is for the amino and carboxyl termini to reside in the cytosol, and for the conserved region to associate with the lipid bilayer. For Rtn1-A, there is experimental evidence demonstrating that the polypeptide behaves as an integral membrane protein, and that the hydrophobic segments of the conserved domain are responsible for this behavior (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416). Myc-tagged Nogo is also associated with particulate fractions and is extracted by detergent but not high ionic strength (data not shown).

When overexpressed in kidney cells, the Rtn1 protein is localized primarily to endoplasmic reticulum (ER) in a finely granulated pattern, hence the Reticulon name (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416). There is a di-lysine ER retention motif at the carboxyl terminus of Nogo and most Rtn proteins (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416; Jackson *et al.*, (1991) EMBO J. 9, 3153-3162). In neurons, Rtn1 is expressed throughout processes and is concentrated in growth cones (Senden *et al.*, (1996) Eur. J. Cell. Biol. 69, 197-213). Its localization in transfected kidney cells has led to the suggestion that Rtn1 might regulate protein sorting or other aspects of ER function (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416). Both the A and C splice forms of Nogo exhibit a reticular distribution when expressed in COS-7 cells, similar to that of Rtn1-C.

## 20 Example 2 - Polyclonal Antibodies against Nogo

The predicted intra-membrane topology of the two hydrophobic domains of Nogo indicates that the 66 amino acid residues between these segments is localized to the luminal/extracellular face of the membrane. To explore this further, an antiserum directed against the 66 amino acid domain was generated.

25 For antibody production and immunohistology, anti-Myc immunoblots and immunohistology with the 9E10 antibody were obtained as described in Takahashi *et al.*, (1998) Nature Neurosci., 1, 487-493 & Takahashi *et al.*, (1999) Cell, 99, 59-69. The GST-Nogo fusion protein was employed as an immunogen to generate an anti-Nogo rabbit antiserum. Antibody was affinity-purified and utilized at 3 µg/ml for

immunohistology and 1 µg/ml for immunoblots. To assess the specificity of the antiserum, staining was conducted in the presence of GST-Nogo protein at 0.1 mg/ml. For live cell staining, cells were incubated in primary antibody dilutions at 4°C for one hour in Hanks balanced salt solution with 0.05% BSA and 20 mM Na-Hepes (pH 7.3).

- 5 After fixation, bound antibody was detected by incubation with fluorescently labeled secondary antibodies.

The antibody detects a low level of surface expression of this epitope, while the Myc epitope at the carboxyl terminus of expressed Nogo is not detected unless cells are permeabilized. This surface staining was attributed to a minority of Nogo protein  
10 associated with the plasma membrane rather than the ER membrane. This data supports a topographic model wherein the amino and carboxyl termini of the protein reside in the cytoplasm and 66 amino acid of the protein protrude on the luminal-extracellular side of the ER or plasma membrane.

15 Example 3 - Nogo Expression in the Central Nervous System

If Nogo is a major contributor to the axon outgrowth inhibitory characteristics of CNS myelin as compared to PNS myelin (Caroni & Schwab, (1988) J. Cell Biol. 106, 1281-1288; Spillmann *et al.*, (1998) J. Biol. Chem. 73, 19283-19293; Bregman *et al.*, (1995) Nature 378, 498-501), then Nogo should be expressed in adult CNS myelin but not  
20 PNS myelin. Northern blot analysis of Nogo expression was performed using probes derived from the 5' Nogo-A/B-specific region and from the 3' Nogo common region of the cDNA. A single band of about 4.1 kilobase was detected with the 5' probe in adult rat optic nerve total RNA samples, but not sciatic nerve samples. The results indicate that the Nogo-A clone is a full length cDNA, and are consistent with a role for Nogo as a  
25 CNS-myelin-specific axon outgrowth inhibitor. Northern blot analysis with a 3' probe reveals that optic nerve expresses high levels of the Nogo-A mRNA and much lower levels of Nogo-B and Nogo-C. Whole brain expresses both Nogo-A and Nogo-C, but a number of peripheral tissues (including sciatic nerve) express little or no Nogo. Nogo-C/Rtn4-C expression has been demonstrated in skeletal muscle and adipocytes, as

well as in brain (Morris *et al.*, (1991) Biochim. Biophys. Acta 1450, 68-76). Within the Rtn family, optic nerve expression appears to be selective for Nogo, with no detectable expression of Rtn 1 or Rtn 3. Rtn 2 has not been examined.

*In situ* hybridization reveals Nogo mRNA in cells with the morphology of  
 5 oligodendrocytes in adult rat optic nerve and pyramidal tract. Within the brain, Nogo expression is also detected in certain neuronal populations. In contrast to Nogo, Rtn1 and Rtn3 are not expressed in optic nerve but mRNA is detected in certain neuronal populations. Nogo protein localization was analyzed in spinal cord cultures treated with PDGF and low serum to induce oligodendrocyte differentiation, using the anti-Nogo  
 10 antibody and the oligodendrocyte-specific O4 monoclonal antibody. In living cells, both the lumenal-extracellular 66 amino acid loop of Nogo and the O4 antigen are detected on the surface of oligodendrocytes. Approximately half of O4-positive cells in these cultures exhibit Nogo surface staining.

#### 15 Example 4 - Nogo-Mediated Growth Cone Collapse

For all experiments involving cell culture, the following methods were employed. The culture of embryonic chick E10 and E12 dorsal root ganglion explants and dissociated neurons utilized methods described for E7 dorsal root ganglion cultures (Takahashi *et al.*, (1998) Nature Neurosci. 1, 487-493; Takahashi *et al.*, (1999) Cell 99, 59-69; Goshima *et al.*, (1995) Nature 376, 509-514; Jin & Strittmatter, (1997) J. Neurosci. 7, 6256-6263).  
 20 NGF-differentiated PC12 cells were cultured as described (Strittmatter *et al.*, (1994) J. Neurosci. 14, 2327-2338). Embryonic spinal cord explants (rat E10 or chick E5) were cultured for 7-14 days in the presence of PDGF-AA to induce differentiation of some cells into mature oligodendrocytes (Vartanian *et al.*, (1999) Proc. Natl. Acad. Sci. USA 96,  
 25 731-735 ). The procedure for growth cone collapse assays is identical to that for analysis of Sema3A-induced growth cone collapse (Takahashi *et al.*, (1998) Nature Neurosci. 1, 487-493; Takahashi *et al.*, (1999) Cell 99, 59-69; Goshima *et al.*, (1995) Nature 376, 509-514; Jin & Strittmatter, (1997) J. Neurosci. 17, 6256-6263). The method for analysis of total neurite outgrowth has also been described (Goshima *et al.*, (1995) Nature 376,

509-514; Jin & Strittmatter, (1997) *J. Neurosci.* 17, 6256-6263; Strittmatter *et al.*, (1994) *J. Neurosci.* 14, 2327-2338). In outgrowth assays, proteins and peptides were added one hour after plating to minimize any effect on the total number of adherent cells. To test the effect of substrate-bound GST or GST-Nogo, the protein solutions were dried on  
5 poly-L-lysine coated glass, washed and then coated with laminin. For E12 cultures, the neuronal identity of cells was verified by staining with anti-neurofilament antibodies (2H3, Developmental Studies Hybridoma Bank) and neurites were traced by observation of rhodamine-phalloidin staining of F-actin in processes.

The expression of recombinant Nogo in HEK293T cells allows a rigorous test of  
10 whether this protein has axon outgrowth inhibiting effects. Washed membrane fractions from vector- or hNogo-A-Myc-transfected HEK293T cells were added to chick E12 dorsal root ganglion explant cultures. Growth cone morphology was assessed after a thirty minute incubation at 37°C by fixation and rhodamine-phalloidin staining.

The control HEK membranes have no detectable effect on growth cone  
15 morphology. The Nogo-A-containing membrane fractions induced collapse of a majority of dorsal root ganglion growth cones. This growth cone collapse indicates an axon outgrowth inhibiting activity, and Nogo inhibition of axon extension is also demonstrable (see below). The Nogo-C form also exhibits collapse activity, indicating that the shared carboxyl terminus of the protein including the hydrophobic segments and the 66 amino  
20 acid lumenal-extracellular domain contains functionally important residues. Additional inhibitory activity in the amino terminal region of Nogo-A is not excluded by these studies. The sensitivity of more immature explant cultures from E10 chick embryos or from E15 rat embryos (data not shown) is substantially less. The developmental regulation of sensitivity is consistent with experiments using partially purified Nogo  
25 (Bandtlow *et al.*, (1997) *Eur. J. Neurosci.* 9, 2743-2752).

Within the growth cone collapsing Nogo-C protein, the hydrophilic 66 lumenal-extracellular domain seems more likely to interact with the surface of dorsal root ganglion neurons than do the membrane-embedded hydrophobic domains. To test this hypothesis, the 66 amino acid region of hNogo was expressed in and purified from *E. coli*. A majority

of the GST-Nogo fusion protein accumulates in inclusion bodies, but can be recovered by urea extraction. This restricted region of Nogo possesses potent ( $EC_{50} = 50$  nM) growth cone collapsing activity for chick E12 dorsal root ganglion neurons (data not shown). The urea-extracted protein preparation is likely to present only a small fraction of the Nogo  
5 sequence in an active conformation. Therefore, 10% of GST-Nogo that is soluble in *E. coli* was purified using a glutathione-Sepharose resin. This preparation is even more potent than the urea-extracted protein as a collapsing factor, acutely altering growth cone morphology at concentrations as low as 1 nM.

The nanomolar potency is on a par with most known physiologic regulators of  
10 axon guidance. Axon outgrowth from dorsal root ganglion neurons and NGF-differentiated PC12 cells is also blocked by this soluble GST-Nogo protein in nM concentrations (data not shown). When GST-Nogo is bound to substrate surfaces, axonal outgrowth from dorsal root ganglion neurons or PC12 cells is reduced to undetectable levels. These are selective effects on axon outgrowth rather than cell survival since  
15 GST-Nogo does not reduce the number of neurofilament-positive adherent cells ( $137 \pm 24\%$  of GST-treated cultures) nor significantly alter the number of apoptotic nuclei identified by DAPI staining ( $4.0 \pm 1.7\%$  in control cultures and  $5.2 \pm 1.1\%$  in GST-Nogo-treated specimens).

Oligodendrocytes appear to express Nogo selectively amongst the Rtn proteins.  
20 To explore the selectivity of Nogo's role in the inhibition of axonal regeneration, the axon outgrowth inhibiting activity of other Rtn proteins was considered. The predicted luminal-extracellular 66 amino acid fragments of Rtn1, Rtn2 and Rtn3 were expressed as GST fusion proteins and purified in native form. At concentrations in which the Nogo fragment collapses a majority of E12 dorsal root ganglion growth cones, the other Rtn  
25 proteins do not alter growth cone morphology (data not shown). Thus, the axon regeneration inhibiting activity is specific for Nogo in the Rtn family.

#### Example 5 - NgR Peptide Agents

To further define the active domain of Nogo, 25 amino acid residue peptides

corresponding to segments of the 66 amino acid sequence were synthesized. The peptide corresponding to residues 31-55 of the extracellular fragment of Nogo exhibits growth cone collapsing (Figure 2) and outgrowth inhibiting (data not shown) activities at concentrations of 4  $\mu$ M. While this sequence may provide the core of the inhibitory domain, the 66 amino acid fragment is clearly required for full potency. Interestingly, this is the region within the 66 amino acid domain sharing the least similarity to other Rtn proteins, consistent with the other family members being inactive as axon regeneration inhibitors. Indeed, the Rtn1 31-55 amino acid luminal-extracellular peptide exerts no growth cone collapse activity (data not shown).

10       The aforementioned experimental data identifies Nogo as an oligodendrocyte-specific member of the Rtn family and demonstrates that a discrete domain of Nogo can inhibit axon outgrowth. Other Rtn proteins do not possess this activity. The expression of Nogo in oligodendrocytes but not Schwann cells therefore contributes to the failure of axonal regeneration in the adult mammalian CNS as compared to the adult PNS. The relative contribution of Nogo as compared to other CNS myelin components to the non-permissive nature of CNS white matter can now be characterized at a molecular level.

While the current experimental data is consistent with a role for Nogo in blocking adult CNS axonal regeneration after pathologic injury, this may also be related to the physiologic role of Nogo in non-pathologic states. Based on localization studies, other Rtn proteins are thought to play a role in ER function (Van de Velde *et al.*, (1994) J. Cell. Sci. 107, 2403-2416). A majority of Nogo is distributed in a reticular pattern in COS-7 cells and only a minority seems to be accessible at the cell surface.

#### 25   Example 6 - Inhibition of Nogo Activity

The previous examples have shown that a 66 amino acid region near the carboxyl terminus of Nogo inhibits axon outgrowth and is expressed at the cell surface. Shorter twenty-five amino acid segments of this domain are either inert as outgrowth inhibitors or of much lower potency (GrandPré *et al.*, (2000) Nature 403, 439-444). The 31-55 region



from this 66 amino acid segment has weak growth cone collapse and axon outgrowth inhibiting activity. To block Nogo action *in vivo*, a competitive antagonist of Nogo which binds to the same receptor site but does not exert a biological effect in its own right would be highly desirable. Various fragments of the 66 amino acid region were tested as

5 blockers of Nogo-mediated axon growth inhibition. Two assays have been used for this purpose. The first is the growth cone collapse assay and the second is a binding assay.

In the growth cone collapse assay, the response to Nogo was measured in the presence of various potential antagonistic peptides. Three of the twenty-five amino acid peptides (1-25, 11-35 and 21-45) from the 66 amino acid region possess blocking activity

10 at  $\mu\text{M}$  concentrations (Figure 2). The combination of all three peptides does not alter growth cone morphology under basal conditions but totally prevents collapse by 15 nM GST-Nogo. The same mixture of peptides is also capable of blocking low dose CNS myelin induced growth cone collapse. This blockade supports the hypothesis that Nogo is a primary inhibitory component of CNS myelin. Furthermore, the blockade has properties

15 expected for competitive antagonism, being ineffective at high doses of CNS myelin.

To develop an antagonist with higher specificity and potency, a longer fragment of Nogo has been tested. Preferentially, such a peptide itself has no axon outgrowth inhibiting activity on its own while competitively blocking Nogo action. The 2-41 fragment of Nogo is acetylated at the carboxy terminus and amidated at the amino

20 terminous and is the highest potency blocker of Nogo defined to date. Pep2-41 abolishes GST-Nogo-induced growth cone collapse and possesses an apparent  $K_i$  of 150 nM in the binding assay (Figure 3). The 2-41 fragment also blocks the ability of both purified Nogo-66 protein and crude CNS myelin to inhibit neurite outgrowth in cultured neurons (Figure 4).

25

#### Example 7 - Identification of the NgR

A Nogo binding assay was developed which utilizes a method widely used in examining semaphorin and ephrin axonal guidance function (Flanagan & Vanderhaeghen, (1998) *Annu. Rev. Neurosci.* 21, 309-345; Takahashi *et al.*, (1999) *Cell* 99, 59-69). It

involves fusing a secreted placental alkaline phosphatase (AP) moiety to the ligand in question to provide a biologically active receptor binding agent which can be detected with an extremely sensitive colorimetric assay. For Nogo, an expression vector was created encoding a signal peptide, a His6 tag for purification, AP and the 66 amino acid active domain of Nogo. The fusion protein can be purified from the conditioned medium of transfected cells in milligram amounts (Figure 5). This protein is biologically active as a growth cone collapsing agent, with an  $EC_{50}$  of 1 nM. AP-Nogo is actually slightly more potent than GST-Nogo perhaps because the protein is synthesized in eukaryotic rather than a prokaryotic cell. Initial studies have revealed saturable, high affinity sites on axons.

Binding is blocked by GST-Nogo and by the antagonistic 25 amino acid peptides, consistent with competitive binding to a neuronal receptor site. Since the apparent  $K_d$  (3 nM) for these sites is close to the  $EC_{50}$  of AP-Nogo in the collapse assay, the sites are likely to be physiologically relevant NgRs.

This assay was utilized for expression cloning of a NgR. Pools of a mouse adult brain cDNA expression library representing 250,000 independent clones were transfected into non-neuronal COS-7 cells. Non-transfected COS-7 cells do not bind AP-Nogo, but transfection with two pools of 5,000 clones exhibited a few cells with strong AP-Nogo binding. Single cDNA clones encoding a Nogo binding site were isolated by sib-selection from each of the two positive pools. The two independently isolated clones are identical to one another except for a 100 bp extension of the 5' untranslated region in one clone. Transfection of these clones into COS-7 cells yields a binding site with an affinity for AP-Nogo identical to that observed in E13 dorsal root ganglion neurons; the  $K_d$  for binding is about 3 nM (Figure 6). AP alone does not bind with any detectable affinity to these transfected cells, indicating that the affinity is due to the 66 amino acid derived from Nogo. Furthermore, GST-Nogo displaces AP-Nogo from these sites.

This cDNA encodes a novel 473 amino acid protein. There is no reported cDNA with significant homology in GenBank. The predicted protein contains a signal peptide followed by eight leucine-rich repeat regions, a unique domain and a predicted GPI anchorage site (Figure 7). A human homologue of the murine cDNA was identified that

- shares 89% amino acid identity. The existence of this cDNA was predicted from the murine cDNA structure and analysis of human genomic sequence deposited in GenBank as part of the Human Sequencing Project. The exons of the human cDNA are distributed over 35 kilobases and the cDNA was not previously recognized in the genomic sequence.
- 5 The protein structure is consistent with a cell surface protein capable of binding Nogo. The GPI-linked nature of the protein suggests that there may be a second receptor subunit that spans the plasma membrane and mediates Nogo signal transduction.

#### Example 8 - Tissue distribution of NgR

- 10 The distribution of the mRNA for this NgR is consistent with a role for the protein in regulating axonal regeneration and plasticity in the adult CNS. Northern analysis shows a single band of 2.3 kilobases in the adult brain, indicating that the isolated NgR clone is full length (Figure 8). Low levels of this mRNA are observed in heart and kidney but not in other peripheral tissues. In the brain, expression is widespread and those areas richest
- 15 in gray matter express the highest levels of the mRNA.

#### Example 9 - Biological effects of different Nogo domains

- Assays of Nogo-A function have included growth cone collapse, neurite outgrowth, and fibroblast spreading with substrate-bound and soluble protein preparations
- 20 (Caroni & Schwab, (1988) J. Cell Biol. 106, 1281-1288; GrandPré *et al.*, (2000) Nature 403, 439-444; Chen *et al.*, (2000) Nature 403, 434-439; Prinjha *et al.*, (2000) Nature 403, 483-484). In assays of 3T3 fibroblast morphology, substrate-bound Nogo-66 does not inhibit spreading (Figure 1b,e). Since NI250 preparations and full length Nogo-A are non-permissive for 3T3 spreading, it was necessary to consider whether different domains
- 25 of Nogo might subserve this *in vitro* activity. To facilitate a comparison of different Nogo-A domains, the acidic amino terminal 1040 amino acid fragment (Amino-Nogo) was expressed as a Myc-his tagged protein in HEK293T cells (Figure 1d). The Nogo protein is present in cytosolic fractions. Surfaces coated with purified Amino-Nogo protein fail to support 3T3 fibroblast spreading (Figure 1b,e). Similar results were

observed for a kidney-derived cell line, COS-7 (Figure 1f). Therefore, the amino terminal domain appears to account for the effects of full-length Nogo-A on fibroblasts. The Nogo-66 domain is specific for neurons; it does not affect non-neuronal cells.

Dorsal root ganglion cultures were also exposed to Amino-Nogo protein (Figure 1c,g-i). As for 3T3 fibroblasts, the fibroblast-like cells in the dorsal root ganglion culture do not spread on this substrate. Furthermore, axonal outgrowth is reduced to low levels on Amino-Nogo coated surfaces. Thus, while the Nogo-66 effects are neural-specific, the inhibitory action of the Amino-Nogo domain is more generalized. When presented in soluble form at 100 nM, the Nogo-66 polypeptide collapses chick E12 dorsal root ganglion growth cones and nearly abolishes axonal extension, as described previously (GrandPré *et al.*, (2000) Nature 403, 439-444). In marked contrast, the soluble Amino-Nogo protein appears inactive, and does not significantly modulate dorsal root ganglion growth cone morphology or dorsal root ganglion axonal extension or non-neuronal cell spreading (Figure 1c,g-i).

In the experiments of Walsh and colleague (Prinjha *et al.*, (2000) Nature 403, 483-484), cerebellar granule neurons were studied and soluble Amino-Nogo was presented as an Fc fusion protein, presumably in dimeric form. Therefore, it was necessary to consider whether these differences might explain the inactivity of soluble Amino-Nogo. Mouse P4 cerebellar granule neurons respond to Nogo preparations in a fashion indistinguishable from chick E13 dorsal root ganglion neurons (Figure 1i). Amino-Nogo dimerized with anti-Myc antibody inhibits 3T3 and COS-7 spreading (Figure 1e,f) and tends to reduce cerebellar axon outgrowth (Figure 1i). When further aggregated by the addition of anti-Mouse IgG antibody, Amino-Nogo significantly reduces both dorsal root ganglion and cerebellar axon outgrowth (Figure 1h,i). While the Amino-Nogo protein is quite acidic, electrostatic charge alone does not account for its inhibitory effects since poly-Asp does not alter cell spreading or axonal outgrowth (Figure 1e,f,h). Thus, the Nogo-66 domain is a potent and neuron-specific inhibitor, while the intracellular Amino-Nogo domain inhibits multiple cell types and appears to function only in an aggregated state.

#### Example 10 - Localization of NgR

To further characterize the expression of the Nogo-66 receptor protein an antiserum to a GST-NgR fusion protein was developed. This antiserum detects an 85 kDa protein selectively in Nogo-66 receptor-expressing HEK293T cells (Figure 9a), and  
 5 specifically stains COS-7 cells expressing Nogo-66 receptor (Figure 9b). Immunohistologic staining of chick embryonic spinal cord cultures localizes the protein to axons, consistent with mediation of Nogo-66-induced axon outgrowth inhibition. Nogo-66 receptor expression is not found in the O4-positive oligodendrocytes that express Nogo-66. Immunoreactive 85 kDa protein is expressed in Nogo-66-responsive neuronal  
 10 preparations from chick E13 dorsal root ganglion, but to a much lesser degree in weakly responsive tissue from chick E7 dorsal root ganglion and chick E7 retina (Figure 9a). Overall, the pattern of Nogo-66 expression is consistent with the protein mediating Nogo-66 axon inhibition.

This antibody is also effective in localizing the Nogo-66 receptor protein in tissue  
 15 sections (Figure 9c). While it is clear from *in situ* hybridization studies that the protein is expressed in multiple classes of neurons, immunohistology reveals the protein at high levels in CNS white matter in profiles consistent with axons. Protein is detectable at lower levels in neuronal soma and neuropil. This provides further support for the proposed function of this protein in mediating interactions with oligodendrocytes.

20

#### Example 11 - NgR mediates Nogo-66 responses

The Nogo-66 receptor protein is necessary for Nogo-66 action and not simply a binding site with a function unrelated to inhibition of axonal outgrowth. A first prediction is that phosphoinositol specific-Phospholipase C (PI-PLC) treatment to remove  
 25 glycoposphatidylinositol (GPI) -linked proteins from the neuronal surface will render neurons insensitive to Nogo-66. This prediction holds true for chick E13 dorsal root ganglion neurons; PI-PLC treatment abolishes both AP-Nogo binding and GST-Nogo-66-induced growth cone collapse (Figure 10a-c). As a control, Sema3A responses in the parallel cultures are not altered by PI-PLC treatment. Of course, PI-PLC

treatment is expected to remove a number of proteins from the axonal surface so this result leaves open the possibility that other GPI-linked proteins are mediating the Nogo-66 response in untreated cultures.

To demonstrate that the Nogo-66 receptor is capable of mediating Nogo-66 inhibition of axon outgrowth, the protein was expressed in neurons lacking a Nogo-66 response. Both dorsal root ganglion and retinal neurons from E7 chick embryos were examined. The Nogo responses in the dorsal root ganglion neurons from this developmental stage are weak but slight responses can be detected in some cultures (data not shown). E7 retinal ganglion cell growth cones are uniformly insensitive to Nogo-66-induced growth cone collapse (Figure 10e), do not bind AP-Nogo (data not shown) and do not exhibit 85 kDa anti-Nogo-66 receptor immunoreactive protein (Figure 9a). Expression of NgR in these neurons by infection with recombinant HSV preparations renders the retinal ganglion cell axonal growth cones sensitive to Nogo-66-induced collapse. Infection with a control PlexinA1-expressing control HSV preparation does not alter Nogo responses. Taken together, these data indicate that the NgR identified here participates in Nogo-66 inhibition of axon regeneration.

#### Example 12 - Structural analysis of Nogo-66 receptor

The Nogo-66 receptor structure was examined to determine which regions mediate Nogo-66 binding. The protein is simply divided into the leucine rich repeat and the non-leucine rich repeat region. Deletion analysis clearly shows that the leucine rich repeats are required for Nogo-66 binding but the remainder of the protein is not necessary (Figure 11). Within the leucine rich repeat domain, two domains have been separately deleted. This is predicted to maintain the overall leucine rich repeat domain structure, and a similar approach has been utilized for the leutropin receptor. It is apparent that the Nogo-66 binding requires all eight leucine rich repeats, and suggests that a significant segment of the planar surface created by the linear beta sheets of the leucine rich repeats. The leucine rich repeat-amino terminous and leucine rich repeat-carboxy terminous conserved cysteine rich regions at each end of the leucine rich repeats are also required for

Nogo-66 binding, presumably these are necessary to generate appropriate leucine rich repeat conformation.

**Example 13 - Blockade of Nogo by soluble NgR ectodomain protein**

- 5           One method for blocking a signal transduction cascade initiated by Nogo-66 binding to the NgR is to provide excess soluble ectodomain of the receptor. A secreted fragment of the NgR protein has been produced in HEK293T cells. The cDNA encoding amino acid residues 1-348 of the murine NgR were ligated into a eukaryotic expression vector and that DNA was transfected into HEK293T cells. Conditioned medium from
- 10 these cells contains high levels of this NgR fragment (NgR-ecto), as demonstrated by immunoblots with an anti-NgR antibody. The conditioned medium contains approximately 1 mg of NgR-ecto protein per liter. In the AP-Nogo binding assay to COS-7 cells expressing full length NgR or to dorsal root ganglion neurons, the addition of NgR-ecto conditioned medium reduces the binding of 0.5 nM AP-Nogo-66 by 80%.
- 15 Complex formation between soluble NgR-ecto and Nogo-66 prevents binding to cell surface receptors.

- For some receptor systems, such soluble receptor ligand complexes can block signaling by creating an ineffective interaction. For example, the soluble ectodomain of Trk serves to block neurotrophin signaling and has been extensively used for this purpose
- 20 (Shelton *et al.*, (1995) *J. Neurosci.* 15, 477-491). Alternatively, the Nogo-66/NgR-ecto soluble complex may bind to and stimulate the presumed second transmembrane NgR subunit. There is precedence for this type of effect from studies of GDNF family receptors (Cacalano *et al.*, (1998) *Neuron* 21, 53-62). The Nogo-66/NgR-ecto complex does not cause growth cone collapse in those neurons (chick E7 retinal ganglion cells)
- 25 which lack the Nogo-66 receptor but containing other components of the Nogo signaling pathway. This indicates that NgR-ecto functions as a blocker of Nogo-66 signaling.

In direct tests, the NgR-ecto protein protects axons from the inhibitory effects of Nogo-66. NgR-ecto prevents Nogo-66-induced growth cone collapse and blocks Nogo-66-induced inhibition of neurite outgrowth from chick E13 DRG neurons (Figure

12). Furthermore, the presence of NgR-ecto protein blocks the ability of CNS myelin to inhibit axonal outgrowth in vitro (Figure 12). These data demonstrate that a NgR-ecto protein can promote axonal regeneration *in vivo*.

5    **Example 14 - Regions in the luminal/extracellular domain of Nogo necessary for NgR binding**

         Portions of the luminal/extracellular domain of Nogo were tested to determine the amino acid sequences responsible for conveying inhibitory activity. To accomplish this, five 25 residue peptides, consisting of overlapping segments of the luminal/extracellular  
10    sequence fused to AP were constructed for testing in binding, growth cone collapse and neurite outgrowth assays.

         To generate AP-fusion proteins, PCR from cDNA of human Nogo-A was used to obtain inserts encoding residues #1055-1094, 1055-1089, 1055-1084, 1055-1079, 1060-1094, 1065-1094 or 1070-1094 of hNogoA (designated 1-40, 1-35, 1-30, 1-25, 6-40,  
15    11-40, 16-40 in Figure 5a). See Figure 13a for the amino acid sequence of each. The inserts were excised and subcloned into the mammalian expression vector pcAP-6. Approximately 60 hours after constructs were transfected into 293T cells, conditioned medium was collected. The concentration of soluble AP-fused proteins within the conditioned medium or the presence of AP-fusion proteins within the conditioned  
20    medium from these cells was verified by measuring AP activity with the substrate *p*-nitro-phenyl phosphate, pNPP, or by western, respectively.

         To determine if AP-fused deletion mutants of Nogo-66 bind mouse NgR ("mNgR"), COS-7 cells were transfected with a plasmid encoding the mouse NgR sequence ligated into pcDNA3.1. 48 hours after transfection, cells were washed with  
25    HBH (Hanks balanced salt solution containing 20 mM sodium Hepes, pH 7.05, and 1 mg ml<sup>-1</sup> bovine serum albumin) and then incubated with condition medium containing one of the AP-fusion proteins described above for 2 hours at 37°C. Cells were then washed, fixed, and left in HBH at 67°C for 14-16 h to inactivate endogenous AP. AP-fusion protein binding to NgR expressing COS-7 cells was detected with the substrates NBT and



BCIP (Figure 13b).

Using this assay, AP fused Nogo-66 has been shown to bind COS7 cells expressing NgR with a  $K_d$  of approximately 7 nM. Equally high affinity binding to NgR expressing cells, but not to non-transfected cells, was obtained with an AP-fusion protein  
 5 consisting of residues 1-40 of the Nogo-66 sequence (designated 140-AP in Figure 14a).

Figure 14b graphically depicts the binding of 140-AP to COS-7 cells expressing mNgR as measured as a function of 140-AP concentration. A plot of the bound/free versus free 140-AP indicates that the  $K_d$  of 140-AP binding to mNgR in this assay is 8nM. See Figure 14c.

10 AP-fusion proteins 1-35 and 6-40 also demonstrated binding to mNgR transfected cells (Figure 13b). Application of AP to these cells does not result in any detectable binding indicating that binding is the result of the Nogo-66 derived residues that were tested. Subsequent experiments (data not shown) have demonstrated that peptides having residues 1-35 and 1-34 bind strongly and almost equivalently to mNgR, whereas peptides  
 15 having residues 1-33 bound mNgR approximately 50% less compared to the strong binders. Peptides having residues 1-31 and 1-30 exhibited almost no binding to NgR. Further, peptides having residues 2-40 of the hNogoA(#1055-1120) bound mNgR well whereas peptides having residues 10-40 had no binding and peptides having 6-40 had intermediate binding. Taken together, the data indicates that there are two regions of the  
 20 hNogoA(#1055-1120) sequence that contain residues necessary for binding: residues 2-10 and 31-34, i.e., sequences IYKGVQAI and EELV.

#### Example 15 - Activity of fragments of the luminal/extracellular domain of Nogo

Tests were conducted to determine if the NgR binding observed with various  
 25 fragments of the luminal/extracellular domain of Nogo was correlated with inhibitory activity. E12 chick DRG growth cone collapse and neurite outgrowth assays that have been described previously were used to determine the inhibitory activity of the fragments.

Briefly, for growth cone collapse, DRG explants were plated on plastic chamber slides precoated with 100  $\mu\text{g ml}^{-1}$  poly-L-lysine and 10  $\mu\text{g ml}^{-1}$  laminin. Cultures were

grown 14-16 h prior to treatment.

For neurite outgrowth assays, plastic chamber slides were coated with 100  $\mu\text{g ml}^{-1}$  poly-L-lysine, washed, and dried. 3  $\mu\text{l}$  drops of PBS containing GST-Nogo-66 were spotted and dried. Slides were then rinsed and coated with 10  $\mu\text{g ml}^{-1}$  laminin before  
5 addition of dissociated E12 chick DRGs. AP-fusion proteins were added at the time of cell plating. Cultures were grown for 5-7 h after which neurite outgrowth was assessed.

Out of the AP fusion proteins that bind NgR, only the AP fusion proteins containing residues #1085-1109 of hNogoA were active in these assays (data not shown) thus indicating that residues within this region are critical to the inhibitory activity of the  
10 luminal/extracellular domain of Nogo. However, the activity of the AP fusion protein containing residues #1085-1109 of hNogoA was considerably less than the larger #1055-1120 fragment. These findings indicate that regions outside of residues #1085-1109, but within residues #1055-1120 of hNogoA may be crucial for high affinity binding of the residues #1055-1120 of hNogoA to NgR.

15 To determine the activity of AP-fusion proteins of Example 14, conditioned medium containing AP-fusion proteins were added to cultures at a final concentration of 20 nM. FIGs. 15a and b show that AP fused to residues #1055-1120 of NogoA is a potent growth-cone-collapsing agent (designated AP-Ng-66 in Figure 15a and 1-66 in Figure 15b). Other AP-fusion proteins containing residues #1055-1094, 1055-1089 or 1060-  
20 1094 (designated as 1-40, 1-35 or 6-40, respectively in Figure 15b) did not induce growth cone collapse in this assay.

Although these fusion proteins bind to COS7 cells expressing NgR with high affinity, they fail to induce significant growth cone collapse in E12 chick DRG explant cultures. These peptides exhibit a desirable characteristic for blockers of Nogo activity -  
25 i.e., they themselves do not have inhibitory activity. The fusion of AP with residues #1055-1094 of hNogoA is a good example of a fusion protein that binds with high affinity to COS7 cells expressing NgR, but fails to mediate growth cone collapse. Taken together, these data suggest that high affinity binding to NgR can be dissociated from activation of an inhibitory signal through NgR.

Example 16 - Synthetic peptide 140 is an antagonist against Nogo-66 activity

(a) Growth Cone Collapse

For further testing, a synthetic peptide containing amino acid residues #1055-1094 of hNgR, acetylated at the carboxy terminus and amidated at the amino terminus was used  
5 [hereinafter "Peptide 140"]. As was shown with the AP-fused version of this peptide, application of Peptide 140 does not induce significant growth cone collapse in E12 chick DRG explant cultures. Antagonist of Nogo-66 inhibitory activity may act by competing for, and thereby blocking NgR binding sites. To determine the antagonistic activity of Peptide 140, the above synthetic form of the peptide was added to E12 chick DRG explant  
10 cultures approximately 10 min before application of various concentrations of GST-NogoA (residues #1055-1120), TPA or Sema3A. 30 min later, cultures were fixed and growth cone collapse was assessed following staining with rhodamine-phalloidin. See Figure 16a.

In this assay, Peptide 140 significantly blocks growth cone collapse induced by  
15 residues #1055-1120 fused to GST. Importantly, when Peptide 140 is applied to these cultures in conjunction with other growth cone collapsing agents, TPA or Sema3A, there is no significant reduction in collapse. These findings indicate that the antagonistic activity of Peptide 140 is selective for Nogo inhibitory activity. See Figure 16b-d.

20 (b) Neurite Outgrowth Activity

Peptide 140 was tested for its ability to neutralize neurite outgrowth inhibition caused by the addition of GST fused to residues #1055-1120 of hNogoA (designated Nogo-66 in Figure 16e). Plastic chamber slides were coated with  $100 \mu\text{g ml}^{-1}$  poly-L-lysine, washed, and dried. 3  $\mu\text{l}$  drops of PBS containing GST-hNogoA(residues  
25 #1055-1120) were spotted and dried. Slides were then rinsed and coated with  $10 \mu\text{g ml}^{-1}$  laminin before addition of dissociated E12 chick DRGs. Peptide 140 was added at the time of cell plating. Cultures were grown for 5-7 h after which neurite outgrowth was assessed.

While GST-hNogoA(residues #1055-1120) dramatically reduces growth in these

cultures, application of Peptide 140 alone has no observable effect on neurite outgrowth from these cells. See Figure 16e. However, when cells are grown in the presence of both Peptide 140 and GST-hNogoA(residues #1055-1120), extensive outgrowth is observed. Importantly, challenging GST-hNogoA(residues #1055-1120)-induced activity with a  
5 scrambled version of Peptide 140 [acetyl-SYVKEYAPIFAGKSRGEIKYQSIEIHEAQVRSDDELVQSLN-amide] does not result in blockade of outgrowth inhibition. Taken together, these studies suggest that Peptide 140 can be used as a functional antagonist of inhibitory activity of the luminal/extracellular domain of Nogo. See Figure 16e.

10

Example 17 - Peptide 140 can neutralize the inhibitory activity of CNS myelin at low concentrations, but not high concentrations of CNS myelin

Inhibitory molecules associated with CNS myelin include MAG, chondroitin sulfate proteoglycans, and Nogo. Currently, the relative contribution of each of these  
15 molecules to the non-permissiveness of CNS myelin is largely unknown. To this end, standard in vitro assays were used to determine whether Peptide 140 can neutralize the inhibitory activity of CNS myelin (Figure 17).

To determine the antagonistic activity of Peptide 140 against CNS myelin, the above synthetic peptide was added approximately 10 min before application of CNS  
20 myelin. 30 min later, cultures were fixed and growth cone collapse was assessed following staining with rhodamine-phalloidin. For neurite outgrowth assays, plastic chamber slide were coated with 100  $\mu\text{g ml}^{-1}$  poly-L-lysine, washed, and dried. 3  $\mu\text{l}$  drops of PBS containing CNS myelin were spotted and dried. Slides were then rinsed and coated with 10  $\mu\text{g ml}^{-1}$  laminin before addition of dissociated E12 chick DRGs.  
25 Peptide 140, or the scrambled version of Peptide 140, was added at the time of cell plating. Cultures were grown for 5-7 h after which neurite outgrowth was assessed.

When applied to E12 chick DRG explant cultures, purified CNS myelin potently mediates growth cone collapse. The addition of both Peptide 140 and CNS myelin to these cultures reveals that at higher concentrations of myelin, the peptide had no effect on

inhibitory activity. This result was not necessarily unexpected given that CNS myelin is known to contain inhibitory molecules other than Nogo. However, at the lowest myelin concentrations tested, Peptide 140 reduces myelin induced growth cone collapse to control levels. These data suggest that Nogo may be the only active inhibitor at low  
5 concentrations of myelin (and may therefore be the most potent inhibitor present in CNS myelin).

In addition to mediating growth cone collapse, CNS myelin dramatically reduces neurite outgrowth when applied to dissociated E12 chick DRG cultures. Addition of Peptide 140 to these cultures results in a partial neutralization of this inhibitory activity  
10 when CNS myelin is presented as a bound inhibitor (Figure 17). For example, neurite outgrowth on a 20 ng spot of myelin increases from 35% to 65% (as compared with control outgrowth) following treatment with Peptide 140. Maximal activity of Peptide 140 is obtained at approximately 250 nM and is progressively lost with higher dilutions of the peptide. The scrambled version of Peptide 140 is ineffective at blocking CNS myelin  
15 induced neurite outgrowth inhibition. Taken together, these data suggest that Nogo is an important contributor to the inhibitory activity of CNS myelin. Further, much of the activity of Nogo-A may be attributable to the Nogo-66 inhibitory domain.

Peptide 140 significantly reduces myelin induced growth cone collapse and can partially restore neurite outgrowth in cultures grown on bound CNS myelin. Thus, Nogo  
20 can be a potent inhibitory molecule in CNS myelin.

There has been reports that neutralization of Nogo activity with the monoclonal antibody IN-1, raised against a myelin fraction enriched in Nogo-A, can partially block the inhibitory activity of CNS myelin both in vitro and in vivo. However, interpretation of the results of these studies is complicated by the presence of two inhibitory domains in  
25 Nogo-A (at residues #1055-1120 and the N-terminus of hNogoA) and a lack of information regarding the epitope of Nogo-A recognized by the IN-1 antibody. Further, using IN-1 to probe a Western blot of proteins extracted from spinal cord reveals binding to Nogo-A but also to a number of other unidentified protein species indicating that the antibody is not highly selective for Nogo-A. In contrast, a peptides derived from the

luminal/extracellular domain of Nogo according to this invention selectively block hNogoA activity.

Example 18 - NgR LRR domains are required for binding to Nogo

5 To define residues critical for binding to Nogo-66 [hereinafter, hNogo-A(1055-1120)], mouse NgR (hereinafter mNgR) deletion mutants were generated and tested for their ability to bind hNogo-A(1055-1120). The amino acid sequence of mNgR contains a signal sequence, an amino-terminal region (NT), eight leucine-rich repeat (LRR) domains (LRR 1-8), a LRR carboxy-terminal domain (LRRCT), a unique carboxy terminal domain  
10 (CT), and a GPI anchor domain. A series of mNgR mutant proteins with specific regions deleted was created using PCR-based site-directed mutagenesis (Fig. 1A).

The mNgR (WTNgR) and mNgR deletion mutants were ligated into the vector pSecTag2Hygro (Invitrogen, Buringame, California). The vector adds to each of the proteins a secretion signal, a C-terminal polyhistidine (6xHis) tag, and a C-terminal  
15 epitope recognized by the anti-His (C-term) antibody. wtNgR encodes residues 1 to 473 of mNgR (Fournier et al., Nature 409:341-346, 2001).

The NgR $\Delta$ NT construct encodes residues 58 to 473 of mNgR. The NgR $\Delta$ NT construct was made by using the primers  $\Delta$ LRR-NT5 (5'-  
tgggatccgaacaaaaactcatctcagaagaggatctgctagccagcgaatcttctctcatggc-3') and NgR3X (5'-  
20 ttctcgaggtcagcagggcccaagcactgtcc-3') to amplify a sequence from the wtNgR-pSecTag2Hygro plasmid. The amplified sequence was ligated into the XhoI/BamHI of pSecTag2.

The NgLRR- construct encodes residues 306 to 473 of mNgR. The NgLRR construct was made by using the primers, MycNgR305 (5'-  
25 tgggatccgaacaaaaactcatctcagaagaggatctgctagagggtgtgtgtggcttca-3') and NgR3X (above) to amplify a sequence from the from the wtNgR-pSecTag2Hygro plasmid. The amplified sequence was ligated into the XhoI/BamHI of pSecTag2.

The NgR $\Delta$ CT construct encodes residues 26 to 305 and 443 to 473 of mNgR, thereby including the LRR and GPI regions of mNgR. Primers MycNgR

(tgggatccgaacaaaaactcatctcagaagaggatctgccatgccctggctgtgtgtgct) and 2NgRt313 (ttgcggccgctgaagccacagcacagccctctag) were used to amplify a sequence from the wtNgR-pSecTag2Hygro plasmid. Primers TM/GPI5 (5'-ttgcggccgctgaggggtcaggggctctgcctgct-3') and NgR3X (above) were used to amplify a sequence from the wtNgR-pSecTag2Hygro  
 5 plasmid. The amplified sequences were ligated together at the NotI site and then ligated into the BamHI/XhoI sites of pSecTag2.

The mNgR LLR deletions and NgR $\Delta$ LRRCT deletion mutants were generated using ExSite<sup>TM</sup> PCR-based site-directed mutagenesis kit (Stratagene, La Jolla, CA). Generally, the primers described below were used to amplify a sequence from the wtNgR  
 10 pSecTag2 plasmid. The ends of the amplified products were ligated together. The resulting constructs were transfected into COS-7 cells.

The NgR $\Delta$ 1-2 construct encodes residues 1 to 56 and residues 106 to 473 of mNgR. The primers used for making the NgR $\Delta$ 1-2 construct were DEL LRR (5'PO4) (5'-ggctgggatgccagtgaggcacagc-3') and DEL LRR2 (5' -ctcctggagcaactagatcttagt-3'). The  
 15 NgR $\Delta$ 3-4 construct encodes residues 1 to 105 and residues 155 to 473 of mNgR. The primers used for making the NgR $\Delta$ 3-4 constructs were DEL LRR3 (5'PO4) (5'-ggtcagaccagtgaaggcagcagc-3') and DEL LRR4 (5'-gctctgcagtacctctacctacaa-3'). The NgR $\Delta$ 5-6 construct encodes residues 1 to 153 and residues 203 to 473 of mNgR. The primers used for making the NgR $\Delta$ 5-6 construct were DEL LRR5 (5'PO4) (5'-  
 20 tgctagtccacggaataggccggg-3') and DEL LRR6 (5'PO4) (5'-agtcttgaccgcctctcttgacac-3'). The NgR $\Delta$ 7-8 construct encodes residues 1 to 202 and residues 251 to 473 of mNgR. The primers used to make the NgR $\Delta$ 7-8 construct were DEL LRR7 (5'PO4) (5'-gtgcaggccacggaagcgtgctc-3') and DEL LRR8 (5'-tctctgcagtacctgcgactcaat-3'). The NgR $\Delta$ LRRCT construct encodes residues 1 to 259 and residues 311 to 473 of mNgR. The  
 25 primers used to make the NgR $\Delta$ LRRCT construct were 3DLRR CT (5'-gtggcttcaggacccttcgctccatc-3') and 5 DLRRCT (5' PO4) (5'-gtcattgagtcgcaggtactgcagagacct-3'). Expression of the mNgR mutants in COS-7 cells was verified by SDS-PAGE and immunoblotting (data not shown).

A vector encoding AP-hNogo-A(1055-1120) was constructed as described in

Fournier et al., supra). The vector encoding AP-NgR was made by ligating the mNgR coding sequence from residues 27-451 in frame with the signal sequence-6xHis-placental alkaline phosphatase (AP) sequence of the vector known as pAP-6 (Nakamura et al., Neuron 2: 1093-1100, 1988).

- 5 AP-hNogo-A(1055-1120) was prepared by transfecting the expression plasmid into HEK293T cells and, after four days, collecting the conditioned medium and purifying the secreted AP-hNogo-A(155-1120) protein by Ni<sup>2+</sup> affinity chromatography as described (Nakamura et al., supra).

- To determine whether mNgR or mNgR deletion mutants bound to hNogo-A(1055-1120), wtNgR or mNgR deletion mutants were transfected into COS-7 cells. Forty-eight hours after the transfection, the transfected COS-7 cells were washed with hanks balanced salt solution containing 20mM sodium HEPES, pH 7.05, and 1 mg/ml bovine serum albumin (BSA) [hereinafter "HBH"]. Cells were then incubated for 2 hours at 23°C with a conditioned medium enriched with purified AP-hNogo-A(1055-1120) diluted in HBH. AP-fusion protein was detected as previously described for AP-Sema3A (Takahashi et al., Nature Neurosci. 1:487-493, 1998).
- 10
- 15

- wtNgR and NgR $\Delta$ CT transfected COS-7 cells bound to AP-hNogo-A(1055-1120), but the other deletion mutants did not (Fig. 18B). The AP-hNogo-A(1055-1120) binding pattern indicates that multiple residues within the NgR LRR region are required for AP-Nogo binding. Because the NgR $\Delta$ 1-2, NgR $\Delta$ 3-4, NgR $\Delta$ 5-6, and NgR $\Delta$ 7-8 deletions remove entire LRR domains it is unlikely that the entire tertiary structure of mNgR is disrupted.
- 20

#### Example 19 - The Effect of NgRCT on mediating NgR-dependent Inhibition

- 25 Because the mouse NgRCT domain was determined to be dispensable for hNogo-A(1055-1120) binding, the ability of NgR $\Delta$ CT to mediate Nogo-dependent inhibition was examined. HSVNgR constructs transfected into HEK293T cells mediated the expression of mNgR proteins of the predicted molecular weight, as determined by SDS-PAGE and anti-Myc and anti-NgR immunoblotting (Fig. 19A). Day E7 chick retinal ganglion cells



(RGCs) were grown for 12 hr, then further incubated for 24 hr with HSVNgR preparations. Explants were fixed with 4% paraformaldehyde with 0.1 M PO<sub>4</sub> and 20% sucrose and stained with phalloidin or with anti-myc antibodies. HSVNgR protein expression was detected in axons of infected (RGC) cultures (Fig. 19B).

- 5           Growth cone collapse in response to GST-hNogo-A(1055-1120) was investigated in infected RGC cultures. Retinal explants infected with recombinant viral preparations of PlexinA1 (PlexA1), wild-type NgR (wtNgR), NgRL1 chimeric receptor in which the GPI domain has been replaced by the transmembrane region and cytoplasmic tail from the mouse adhesion protein L1(NgRL1), or NgR carboxy terminal deletion mutant (NgRΔCT)
- 10   for 12 hr. Following infection, the cells were treated for 30 min with 0, 50, 250, or 500 nM GST-hNogo-A(1055-1120) (GrandPre et al., Nature 403: 439–444, 2000), fixed with 4% paraformaldehyde with 0.1 M PO<sub>4</sub> and 20% sucrose, and stained with phalloidin. As shown in Figure 20, cells infected with the control PlexA1 virus did not respond to GST-hNogo-A(1055-1120), whereas cells infected with wtNgR underwent growth cone
- 15   collapse in response to GST-hNogo-A(1055-1120). Cells infected with NgRΔCT were insensitive to GST-hNogo-A(1055-1120). The CT region of NgR is therefore required for effective NgR inhibitory signaling.

#### Example 20 - The Effect of the CT Domain Alone on NgR Inhibitory Signaling

- 20           As NgR is a GPI linked protein tethered to the plasma membrane, it is likely that a second protein exists in a NgR signaling complex that is responsible for transducing Nogo signals within the cell. One possibility is that the CT domain of NgR may bind to a transducing component and initiate an intracellular signaling cascade upon ligand binding. This possibility would be consistent with the signaling incompetence of NgRΔCT. If so,
- 25   it is also possible that the NgR CT region may be capable of constitutive inhibitory activity. To test this possibility, a GSTNgRCT fusion protein was produced by PCR amplifying the CT region of NgR (amino acids 310–450) and ligating the fragment into the BamHI/EcoRI site of pGEX2T. The fusion protein was expressed and tested in a neurite outgrowth assay. E13 chick dorsal root ganglion (DRG) cells were dissociated and

plated in the presence or absence of 100 nM soluble GSTNgRCT and assayed for neurite outgrowth lengths. In this assay, GST-hNogo-A(1055-1120) has been shown to inhibit neurite outgrowth (Fournier et al., supra). Soluble GSTNgRCT did not alter neurite outgrowth lengths, nor did it attenuate or enhance the response of dissociated E13 DRGs to GST-hNogo-A(1055-1120) substrates (Fig. 21).

**Example 21 - The NgR GPI domain is not required for NgR signaling**

To test the possibility that the GPI anchor has a role in mediating inhibitory Nogo signaling, a chimeric NgR molecule was constructed and assessed for its ability to correctly localize within the cell. HSVL1NgR contains a HSVNgR fusion in which the NgR GPI domain is replaced with the transmembrane domain of L1. HEK293T cells were cultured in 6-mm dishes and transfected with HSVwtNgR or HSVL1NgR. After 48 hr, cells were rinsed with PBS and lysed on ice with 375  $\mu$ l precooled buffer containing 50 mM Tris-HCl (pH 7.4), 150 mM NaCl, 5 mM EDTA, and 0.1 % Triton X-100, (hereinafter "TNEX"), and 10 mM NaF and a protease inhibitor cocktail (Roche Diagnostics, Mannheim, Germany). Cells were homogenized by passing the ice-cold lysates through a 27 G needle 10 times. Extracts were adjusted to 35% OptiPrep (Gibco BRL) by adding 525  $\mu$ l of 60% OptiPrep/0.1% Triton X-100, then placed in an ultracentrifuge tube and overlaid with 8.75 ml of 30% OptiPrep in TNEX and 1 ml of TNEX. After centrifugation (4 hr, 200,000 x g, 4°C), seven fractions were collected, precipitated with trichloroacetic acid, washed with acetone, air dried, and resuspended in Laemlli sample buffer. Fractions were analyzed by 8% SDS-PAGE and immunoblotting with the NgR antibody (Fournier et al., supra). Transferrin receptor (TfR) was detected with an anti-TfR monoclonal antibody; caveolin was detected with anti-caveolin rabbit polyclonal antibody.

As expected for a GPI-anchored protein, wtNgR localized mainly to caveolin-rich lipid raft fractions (Fig. 22). A much smaller proportion of the chimeric L1NgR was localized to the lipid raft fraction. Expression of the wild-type HSVNgR or HSVNgRL1chimeric protein in HEK293T cells results in an altered distribution of

HSVNgRL1.

Example 22 - mNgR Binds mNgR

NgR was tested for the ability to self-associate. For this study, mNgR [hereinafter, wtNgR or WT] and mNgR deletion mutants (see Fig. 18A) were transfected into COS-7 cells. Forty-eight hours after the transfection, the transfected COS-7 cells were washed with HBH. Cells were then incubated for 2 hours at 23°C with a conditioned medium containing AP-hNogo-A(1055-1120) fusion protein diluted in HBH. AP-fusion protein was detected as previously described for AP-Sema3A (Takahashi et al., Nature Neurosci. 1:487-493, 1998). Similar to the AP-Nogo binding profile, AP-NgR bound to wtNgR and NgRACT (Fig. 23). Nogo treatment had little, if any, effect on the NgR-NgR interaction (data not shown). Other NgR deletion mutants did not bind AP-NgR. The same NgR domains are required for GST-hNogo-A(1055-1120) binding and NgR oligomerization

Example 23 - Soluble NgR antagonizes Nogo and myelin-dependent inhibition

Although the role of the GPI anchor may be to regulate NgR cellular compartmentalization, another possible role for the GPI linkage is to provide a NgR cleavage site. Cleaving NgR could serve to affect hNogo-A(1055-1120) signaling by rendering a neuron insensitive to hNogo-A(1055-1120) and by releasing soluble NgR that could then act on adjacent cells to modulate hNogo-A(1055-1120) signaling. To determine if soluble mNgR modulates hNogo-A(1055-1120)-dependent inhibition, a soluble mNgR was generated by inserting a truncated cDNA encoding mNgR residues 1-348 in frame with a myc-His carboxy tag into pcDNA3.1. The resulting plasmid expressing mNgREcto was transfected into HEK293T cells, and conditioned media containing mNgREcto protein was collected. To test the effect of mNgREcto on Nogo signaling, E13 dissociated DRGs were plated in the presence of hNogo-A(1055-1120) or myelin. The inhibitors were presented in either soluble or substrate-bound forms. For neurite outgrowth assays on hNogo-A(1055-1120) or myelin substrates, Permanox chamber slides were coated with 100  $\mu$ , fs24 g ml<sup>-1</sup> poly-L-Lysine, washed, and then 3- $\mu$ l

drops of phosphate-buffered saline (hereinafter "PBS") containing 0, 10, 50, or 150 ng of GST-hNogo-A(1055-1120) or myelin were spotted and dried. GST-hNogo-A(1055-1120) and myelin were prepared as previously described (GrandPre et al., supra; Fournier et al., J. Cell Biol. 149:411-421, 2000). After three PBS washes, slides were coated with 10  $\mu\text{g ml}^{-1}$  laminin. Laminin was then aspirated and dissociated E13 chick DRG neurons were added. After 6-8 hr of outgrowth, cultures were fixed and neurite outgrowth lengths were assessed. For blockade experiments with NgREcto, spots were incubated with HEK293T cell conditioned media or NgREcto-transfected-HEK293T cell conditioned media following for 1 hr following the laminin coating step and before the addition of dissociated neurons. As shown in Figure 24, following blockage with NgREcto, neurite outgrowth inhibition by Nogo or myelin substrates was partially reversed. Thus, soluble fragments of NgR might serve physiologically or pharmacologically to reduce GST-hNogo-A(1055-1120) inhibition of axonal regeneration.

To test the signaling capability of NgRL1, recombinant HSV1NgR preparations were produced and used to infect E7 RGCs. Infected RGCs were treated with GST-hNogo-A(1055-1120) and growth cone collapse was assessed (Fig. 20). At high concentrations of GST-hNogo-A(1055-1120), NgRL1 transduces Nogo signals as efficiently as wtNgR. However, at 50 nM GST-hNogo-A(1055-1120), wtNgR is capable of signaling whereas NgRL1 infected RGCs are not responsive to GST-hNogo-A(1055-1120). This indicates that NgRL1 is capable of mediating inhibitory signals in response to Nogo, however less efficiently than wtNgR. When transfected HEK293T cells were treated with GST-hNogo-A(1055-1120), the membrane fractionation profile of wtNgR and L1Ngr remained the same (data not shown) suggesting that Nogo does not modulate NgR localization to lipid raft compartments in HEK293T cells. It is however possible that ligand binding to NgR modifies signaling within the compartment as is the case for ephrins (Davy et al., Genes Dev., 13:3125-3135, 1999) or recruits unknown signaling partners to a lipid raft complex. Because the intracellular signals induced by Nogo have not been elucidated, it remains to be determined if ligand binding effects signaling events at caveolar microdomains.

Throughout the specification, the word "comprise," or variations such as "comprises" or "comprising," will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

Although the present invention has been described in detail with reference to  
5 examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Therefore, it will be appreciated that the scope of this invention is encompassed by the embodiments of the inventions recited herein and the specification rather than the specific examples which are exemplified below. All cited patents and publications referred to in this application are herein incorporated by reference  
10 in their entirety. The results of part of the experiments disclosed herein have been published (GrandPré *et al.*, (2000) Nature 403, 439-444) after the filing date of U.S. Provisional Application 60/175,707 from which this application claims priority, this publication herein incorporated by reference in its entirety.

## CLAIMS

What is claimed:

1. A nucleic acid comprising a nucleotide sequence encoding a polypeptide comprising:  
(a) amino acid residues 27-309 of SEQ ID NO:2 (human NgR NTLRRCT domain), or amino acid residues 27-309 of SEQ ID NO:2 with 1-20 conservative amino acid substitutions; and (b) and less than a complete CTS domain, provided that a partial CTS domain, if present, consists of no more than the first 39 consecutive amino acid residues.
2. The nucleic acid of claim 1, wherein the encoded polypeptide comprises amino acid residues 27-309 of SEQ ID NO:2.
3. The nucleic acid of claim 1, wherein the encoded polypeptide comprises fewer than 50 consecutive amino acids from amino acids 310-445 of SEQ ID NO:2.
4. The nucleic acid of claim 1, wherein the encoded polypeptide does not comprise a functional GPI domain.
5. A vector comprising the nucleic acid of claim 1.
6. The vector of claim 5, wherein the nucleic acid is operably linked to an expression control sequence.
7. A cell comprising the vector of claim 5.
8. A polypeptide comprising: (a) amino acid residues 27-309 of SEQ ID NO:2 (human NgR NTLRRCT domain), or amino acid residues 27-309 of SEQ ID NO:2 with 1-20 conservative amino acid substitutions; and (b) fewer than 115 consecutive

amino acids from amino acids 310-445 of SEQ ID NO:2.

9. The polypeptide of claim 8, wherein the polypeptide comprises amino acid residues 27-309 of SEQ ID NO:2.

10. The polypeptide of claim 8, wherein the polypeptide comprises fewer than 50 consecutive amino acids from amino acids 310-445 of SEQ ID NO:2.

11. The polypeptide of claim 8, wherein the encoded polypeptide does not comprise a functional GPI domain.

12. A method of producing the polypeptide of claim 8, comprising introducing a nucleic acid encoding the polypeptide into a host cell, culturing the host cell under conditions suitable for expression of said polypeptide, and recovering the polypeptide.

13. An antibody that binds to an epitope in the CTS domain of NgR.

14. A method of inhibiting binding of a Nogo polypeptide to a NgR, comprising contacting the Nogo polypeptide with an effective amount of the polypeptide of claim 8.

15. A method of inhibiting binding of a Nogo polypeptide to a NgR, comprising contacting the NgR with an antibody that binds to the amino acid sequence consisting of SEQ ID NO:2 (NgR polypeptide).

16. The method of claim 15, wherein the antibody binds to an epitope within amino acids 310-445 of SEQ ID NO:2 (CTS domain of NgR).

17. A method of decreasing inhibition of axonal growth by a CNS neuron, comprising contacting the neuron with an effective amount of a molecule selected from the group consisting of: (a) a polypeptide of claim 8; and (b) an antibody that binds to the amino acid sequence consisting of SEQ ID NO:2 (NgR).

18. The method of claim 17, wherein the antibody binds to an epitope within the amino acid sequence consisting of amino acids 310-445 of SEQ ID NO:2 (CTS domain of NgR).

19. A method of treating a central nervous system disease, disorder or injury, comprising administering to a mammal an effective amount of an agent selected from the group consisting of: (a) an agent that inhibits binding of a Nogo polypeptide to a NgR; and (b) an agent that inhibits NgR-dependent signal transduction in a central nervous system neuron.

20. The method of claim 19, wherein the agent that inhibits binding of a Nogo polypeptide to a NgR is selected from the group consisting of: (a) a polypeptide of claim 8; (b) an antibody that binds to a polypeptide consisting of SEQ ID NO:2.

21. The method of claim 20 wherein the antibody binds to an epitope within the amino acid sequence consisting of amino acids 310-445 of SEQ ID NO:2 (CTS domain of NgR).

22. The method of claim 19, wherein the central nervous system disease, disorder or injury is a spinal cord injury.

23. A method for identifying a molecule that decreases Nogo-dependent inhibition of axonal growth, the method comprising:

(a) providing a NgR polypeptide;



- (b) contacting the NgR polypeptide with a candidate molecule; and
- (c) detecting a decrease in binding of the Nogo polypeptide to the NgR in the presence of the candidate molecule, as compared to the binding of the Nogo polypeptide to the NgR in the absence of the candidate molecule.

24. A composition comprising a polypeptide of claim 8 and a pharmaceutically acceptable carrier.

25. A composition comprising an antibody of claim 13 and a pharmaceutically acceptable carrier.

26. A nucleic acid comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) IYKGVIQAI and (b) EELV, the polypeptide comprising 40 amino acids or fewer.

27. The nucleic acid of claim 26, wherein the polypeptide comprises the amino acid sequences IYKGVIQAI and EELV.

28. The nucleic acid of claim 26, wherein the polypeptide comprises fewer than 40 amino acids.

29. The nucleic acid of claim 28, wherein the polypeptide comprises amino acid residues 2 to 34 of SEQ ID NO:21.

30. The nucleic acid of claim 26, wherein the polypeptide encoded further comprises a heterologous amino acid sequence not present in NogoA, the heterologous amino acid sequence comprising at least five amino acid residues.

31. A polypeptide comprising an amino acid sequence selected from the

group consisting of: (a) IYKGVQAI and (b) EELV, the polypeptide comprising 40 amino acids or fewer.

32. The polypeptide of claim 31, wherein the polypeptide comprises the amino acid sequences IYKGVQAI and EELV.

33. The polypeptide of claim 32, wherein the polypeptide comprises fewer than 40 amino acids.

34. The polypeptide of claim 33, wherein the polypeptide comprises amino acid residues 2 to 34 of SEQ ID NO:21.

35. The polypeptide of claim 31, wherein the polypeptide further comprises a heterologous amino acid sequence not present in NogoA, the heterologous amino acid sequence comprising at least five amino acid residues.

36. An antibody that binds to a polypeptide of claim 31.

37. A composition comprising a polypeptide of claim 31 or an antibody according to claim 36 and a pharmaceutically acceptable carrier.

38. A method of inhibiting binding of a Nogo polypeptide to a NgR, comprising contacting the NgR with an effective amount of the polypeptide of claim 31.

39. A method of inhibiting binding of a Nogo polypeptide to a NgR, comprising contacting the Nogo polypeptide with an effective amount of the antibody according to claim 36.

40. A method of decreasing inhibition of axonal growth by a CNS neuron,

comprising contacting the neuron with an effective amount of a polypeptide of claim 31 or an antibody of claim 36.

41. A method of treating a central nervous system disease, disorder or injury, comprising administering to a mammal an effective amount of a polypeptide of claim 31 or an antibody of claim 36.

42. The method of claim 41, wherein the central nervous system disease, disorder or injury is a spinal cord injury.

43. A method of identifying a molecule that decreases axonal Nogo-dependent inhibition of axonal growth, the method comprising:

- (a) providing a polypeptide comprising a target sequence consisting of an amino acid sequence selected from the group consisting of IYKGVIQAI and EELV;
- (b) contacting the polypeptide with a candidate molecule; and
- (c) detecting binding of the candidate molecule to a target sequence in the polypeptide.

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FIG. 1a

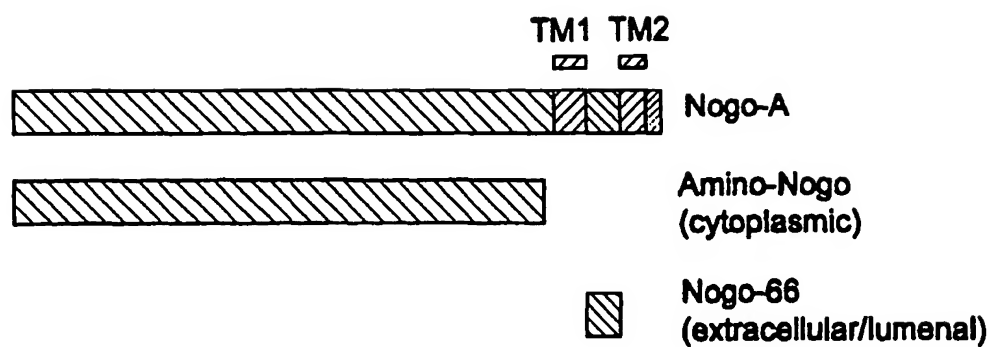
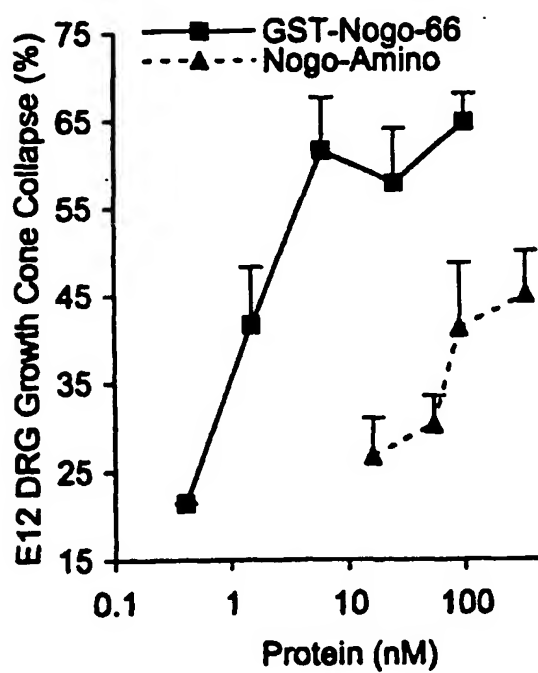


FIG. 1g



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FIG. 1b



FIG. 1c

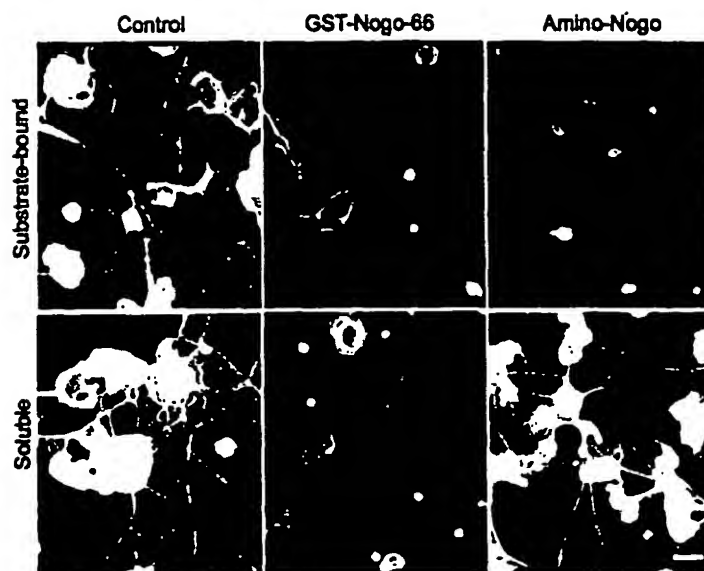
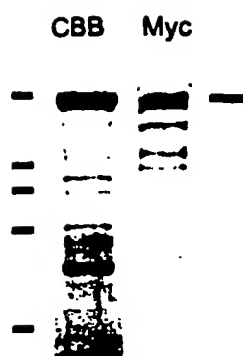
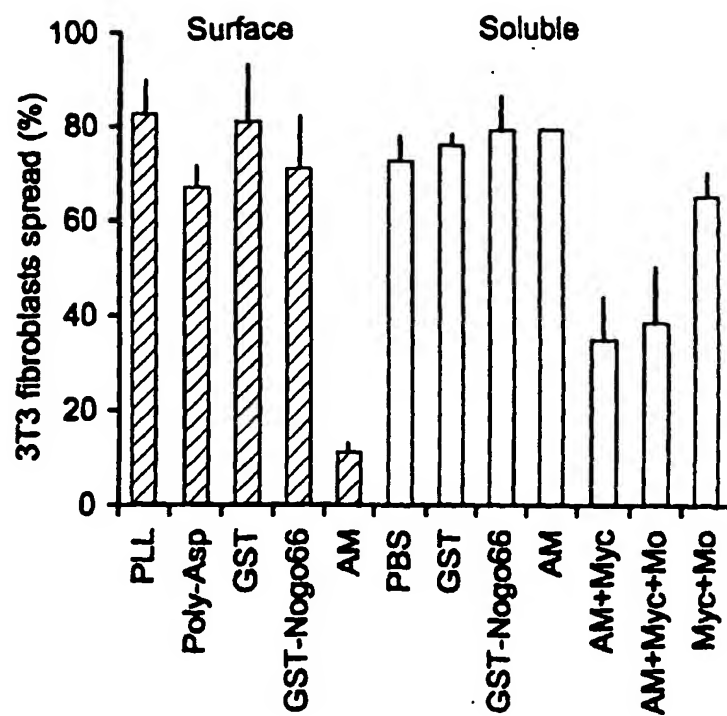
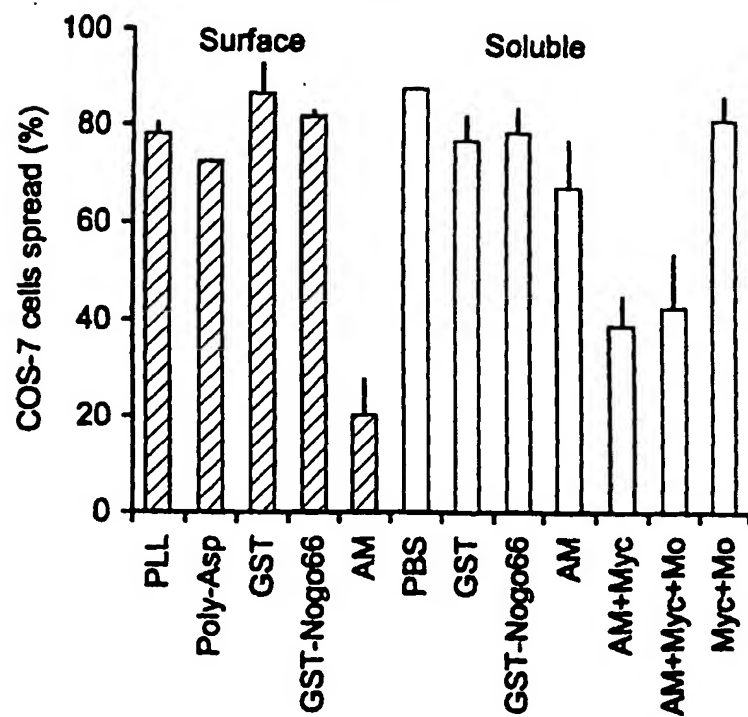


FIG. 1d



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**FIG. 1e****FIG. 1f**

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FIG. 1h

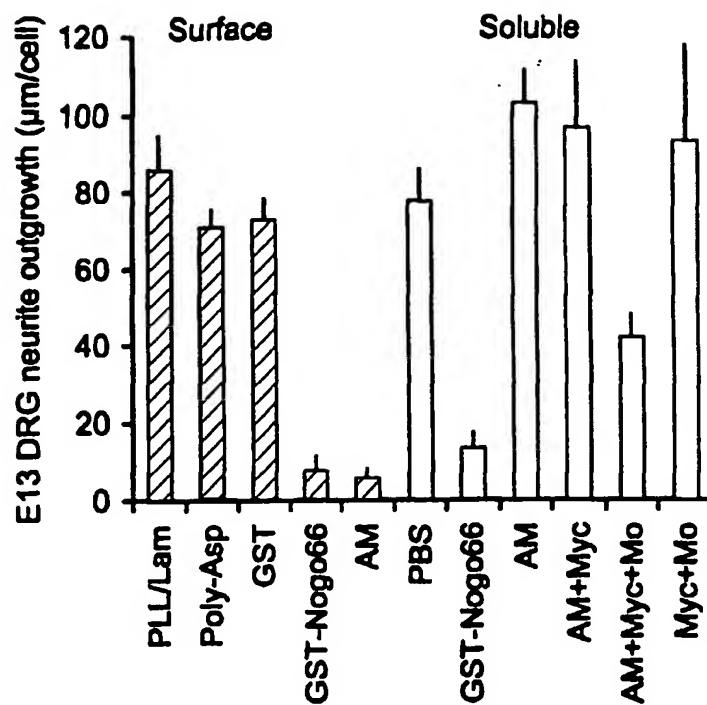
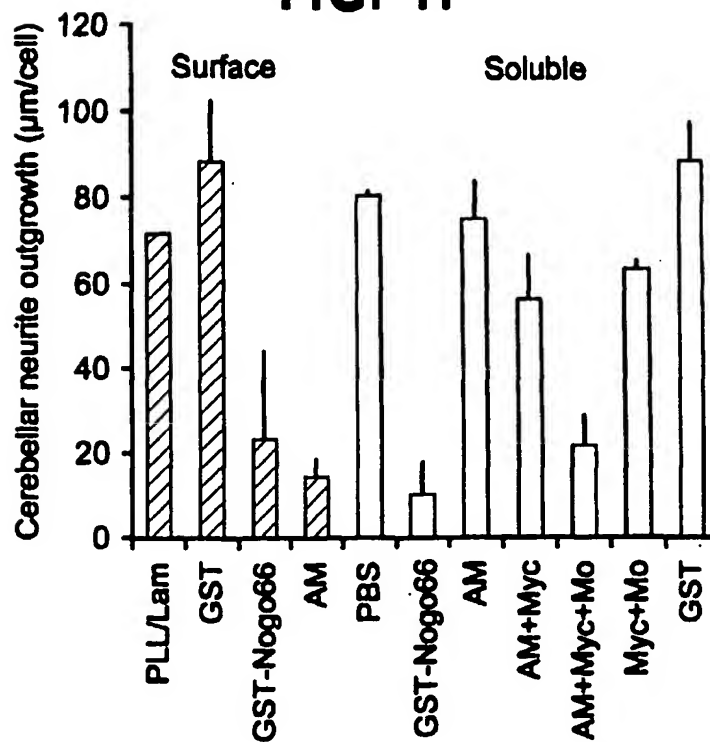


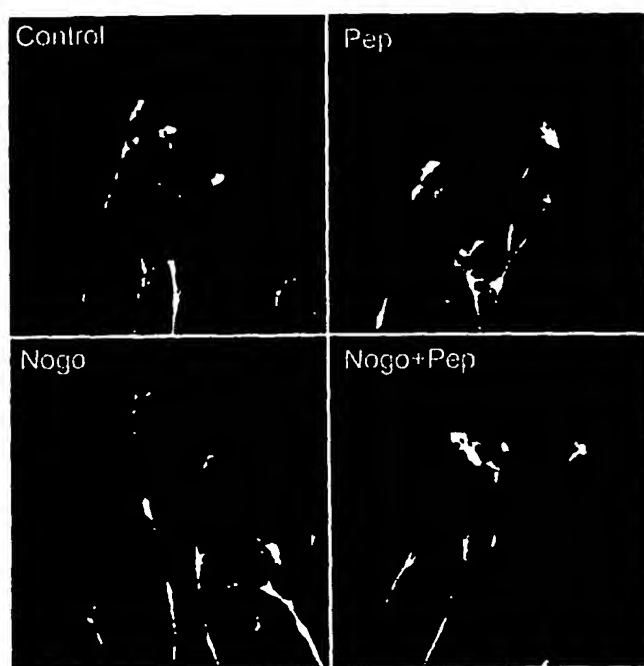
FIG. 1i



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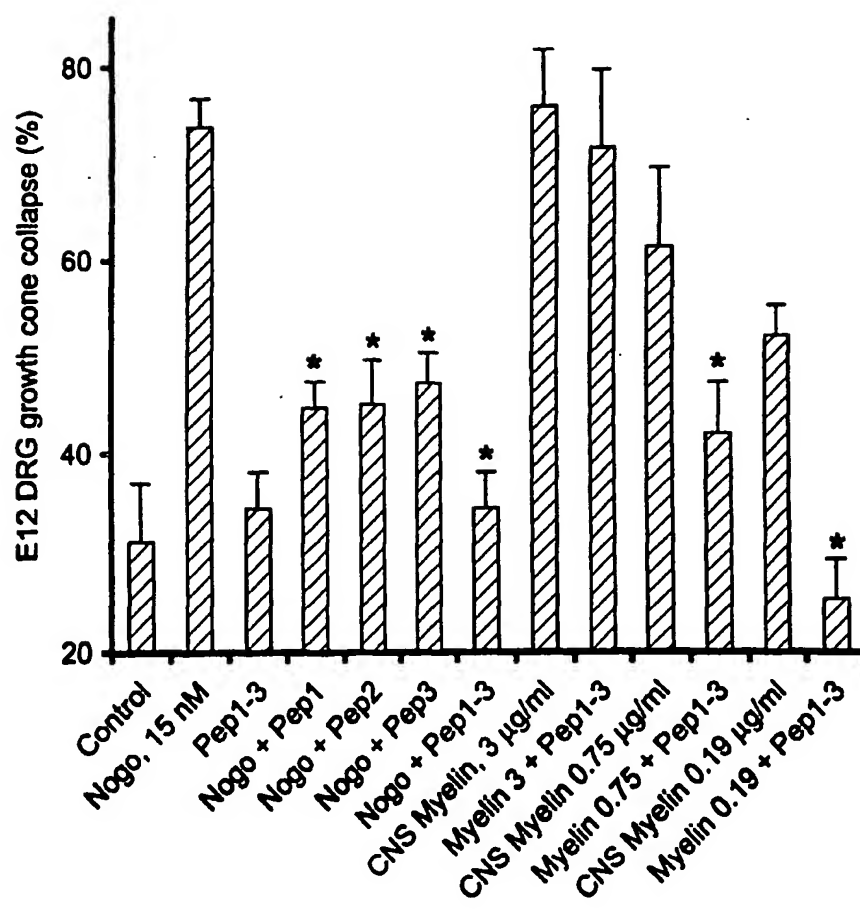
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**FIG. 2A**

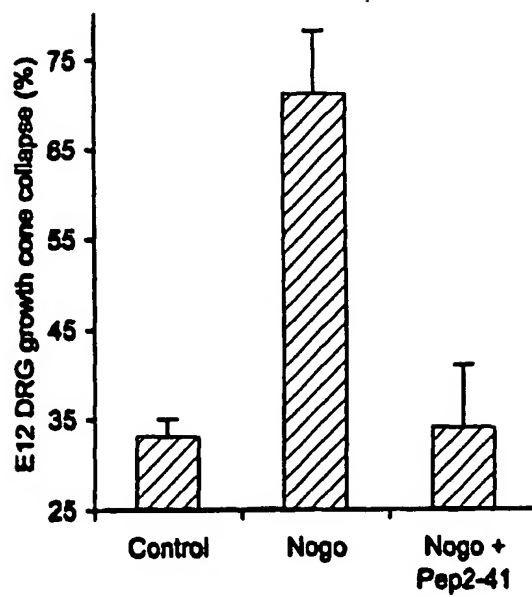
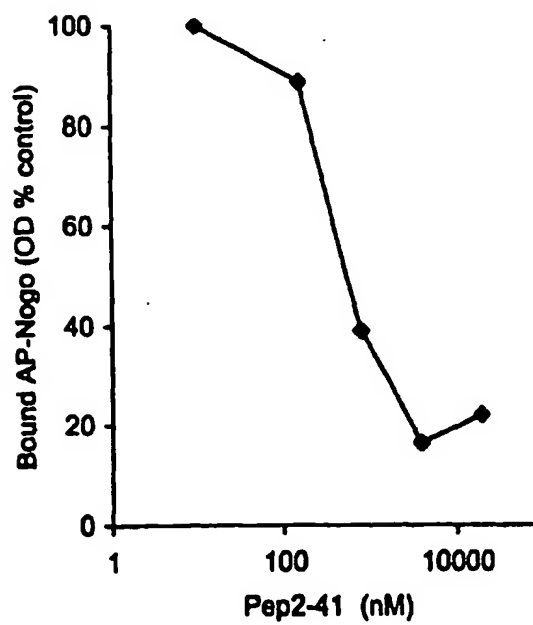




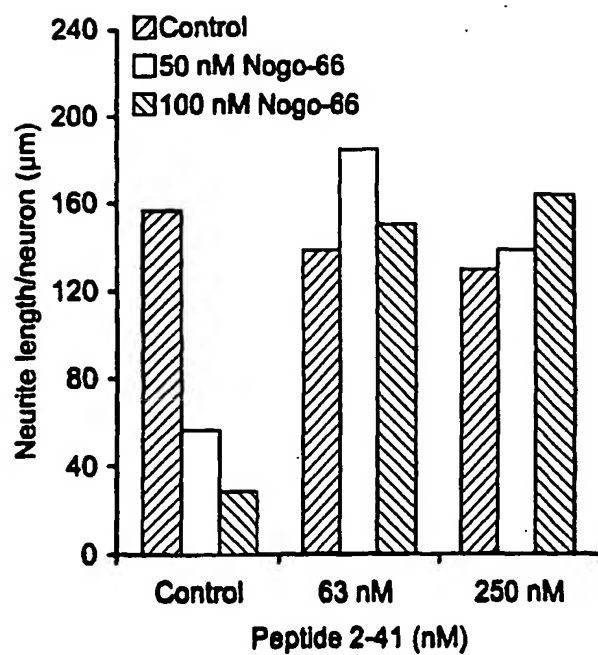
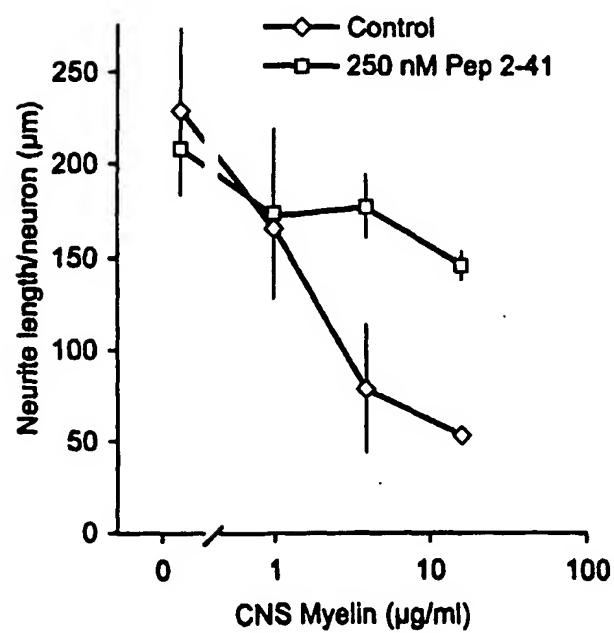
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**FIG. 2B**

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**FIG. 3A****FIG. 3B**

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**FIG. 4A****FIG. 4B**

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**FIG. 5A** **FIG. 5B**



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FIG. 5C

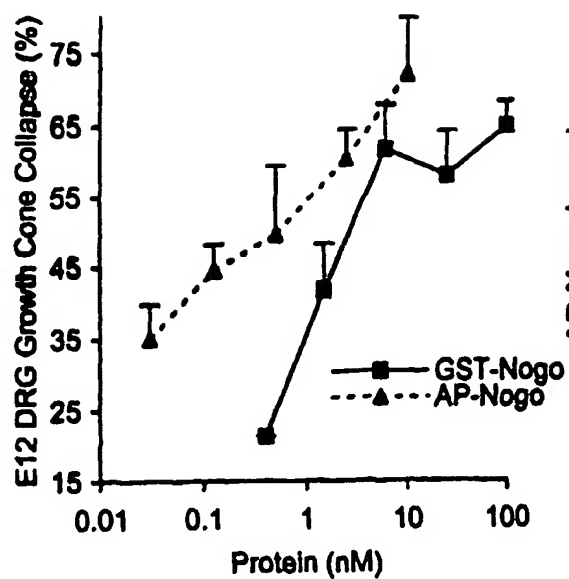


FIG. 5D

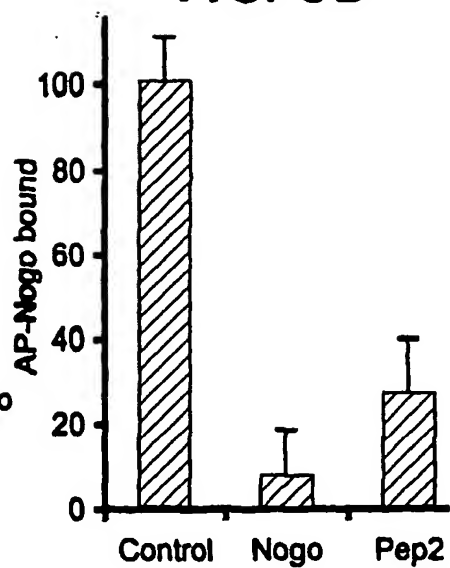


FIG. 5E

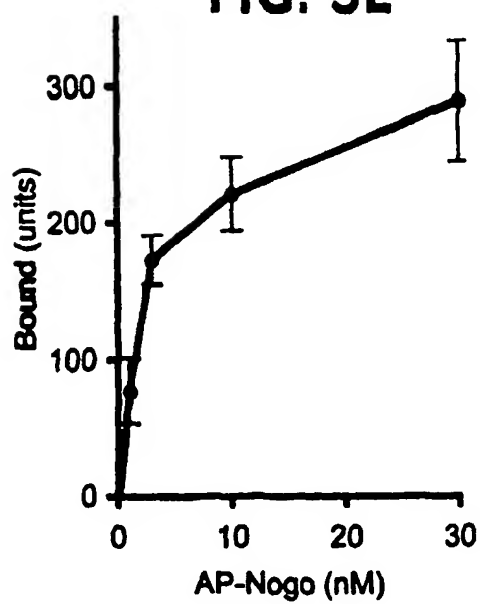
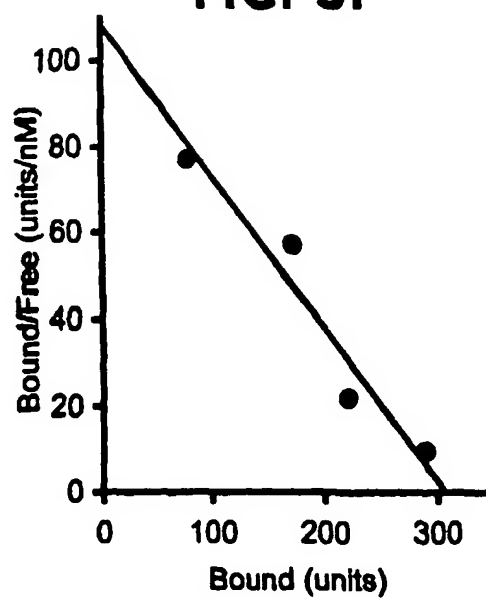


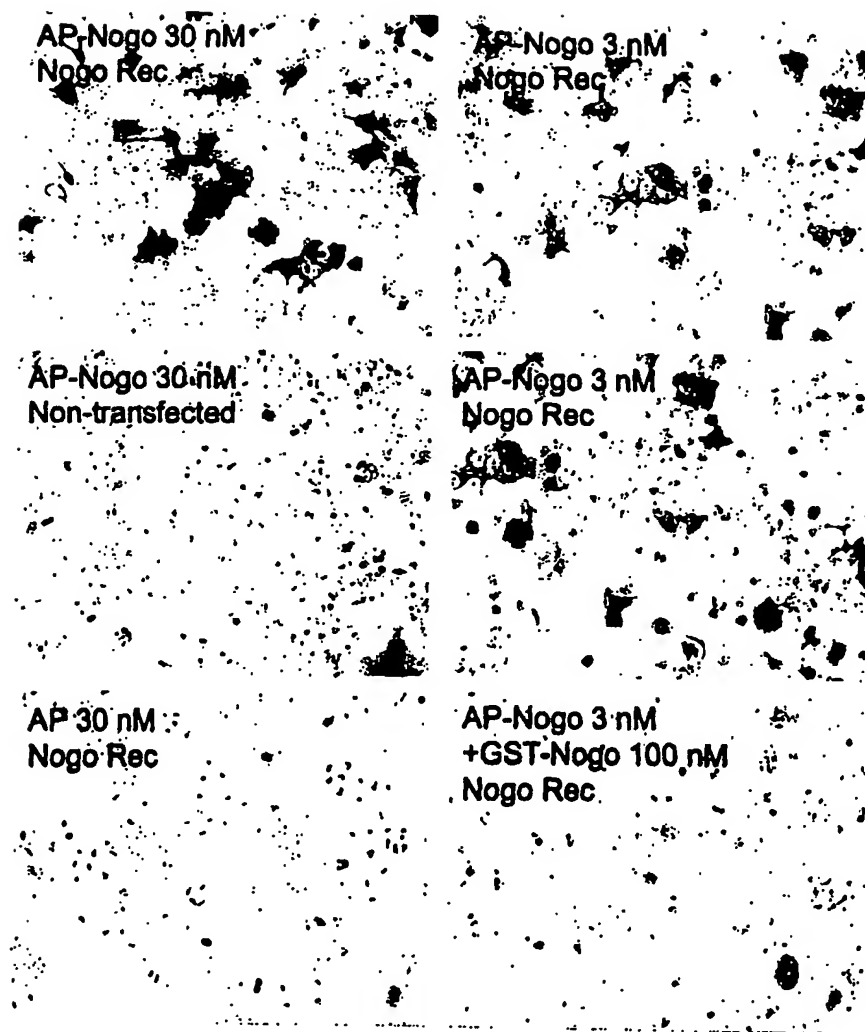
FIG. 5F



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FIG. 6

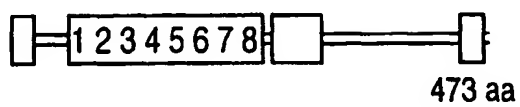


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**FIG. 7**

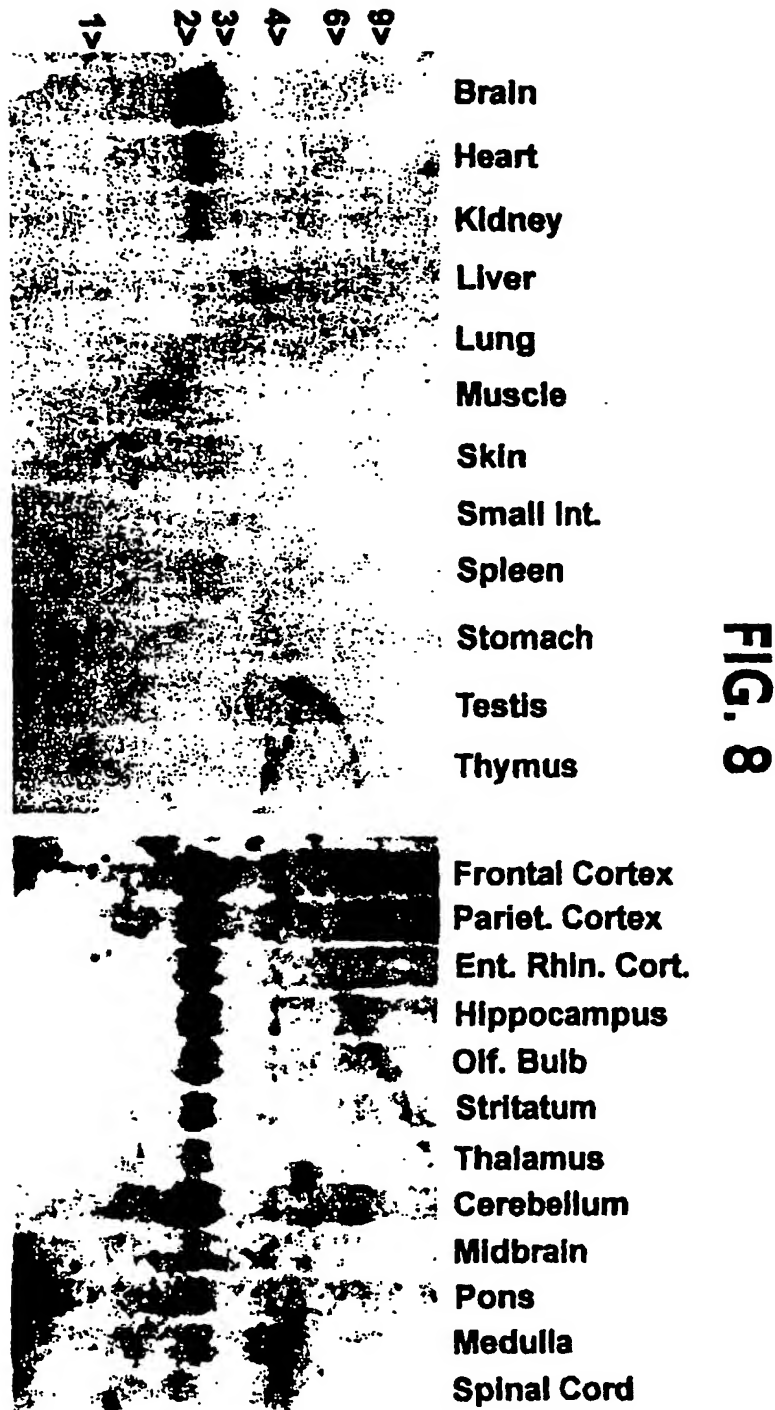
Nogo Receptor

Signal Leu-Rich Rep LRRCT TM/GPI



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FIG. 9B

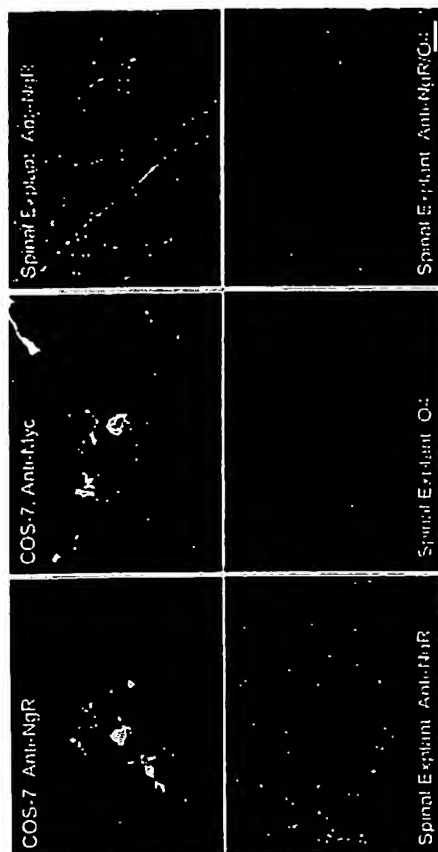


FIG. 9A

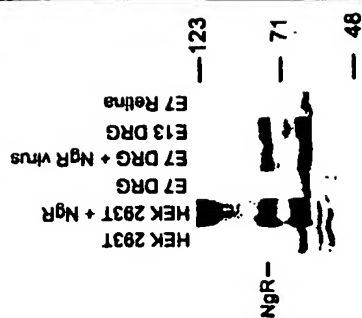


FIG. 9C



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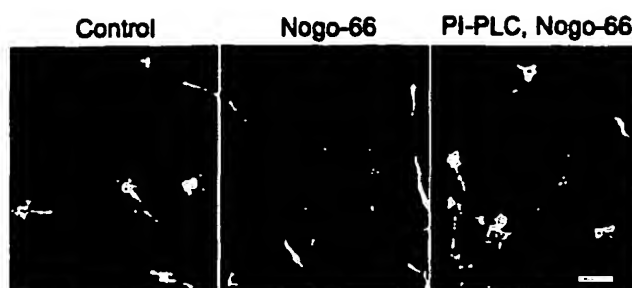
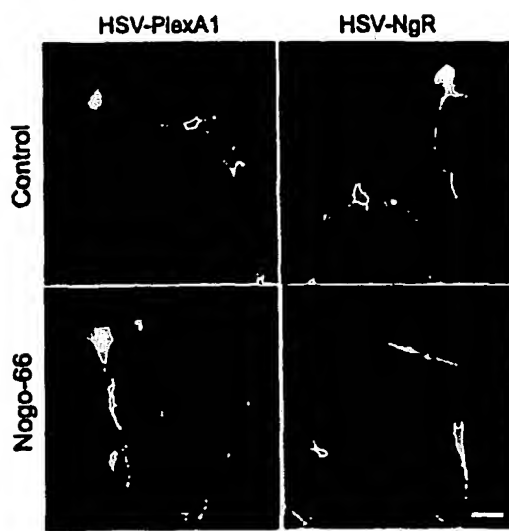
**FIG. 10a****FIG. 10d**

FIG. 10b

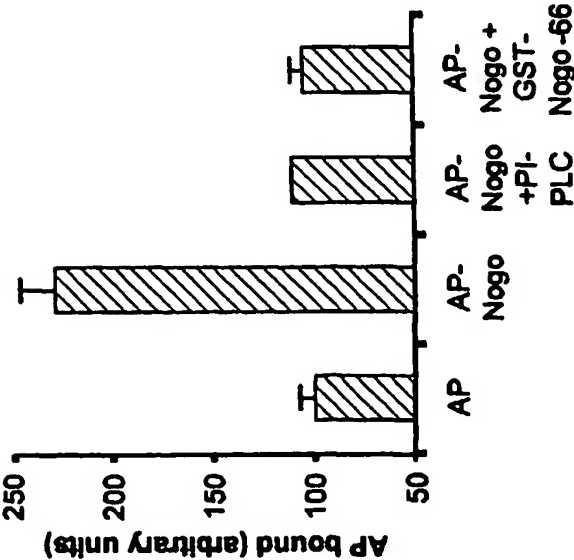


FIG. 10c

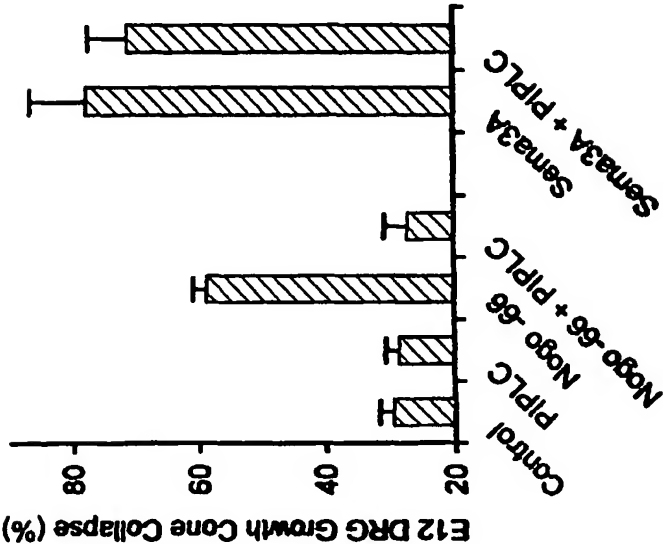
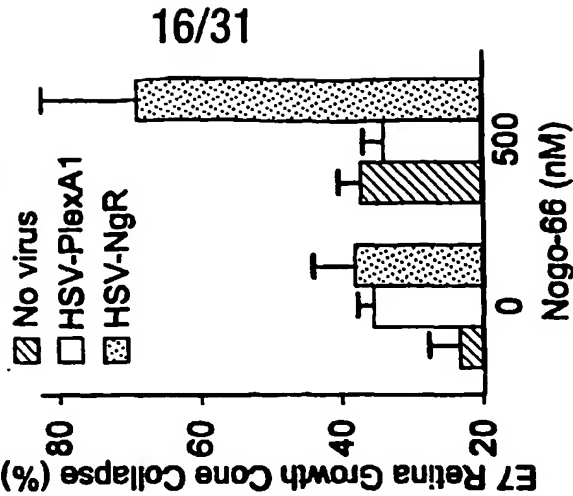


FIG. 10e

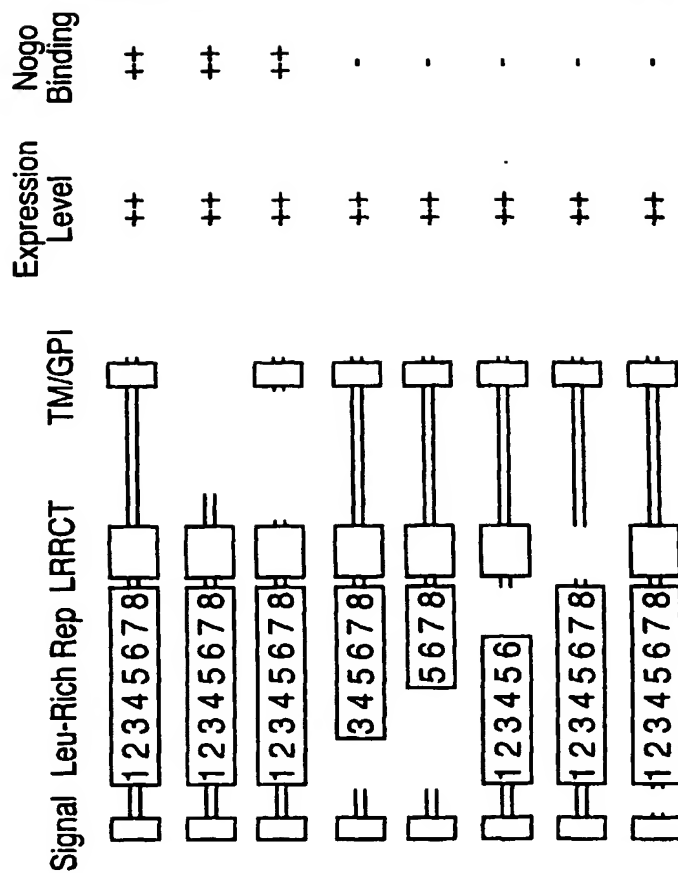


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FIG. 11b

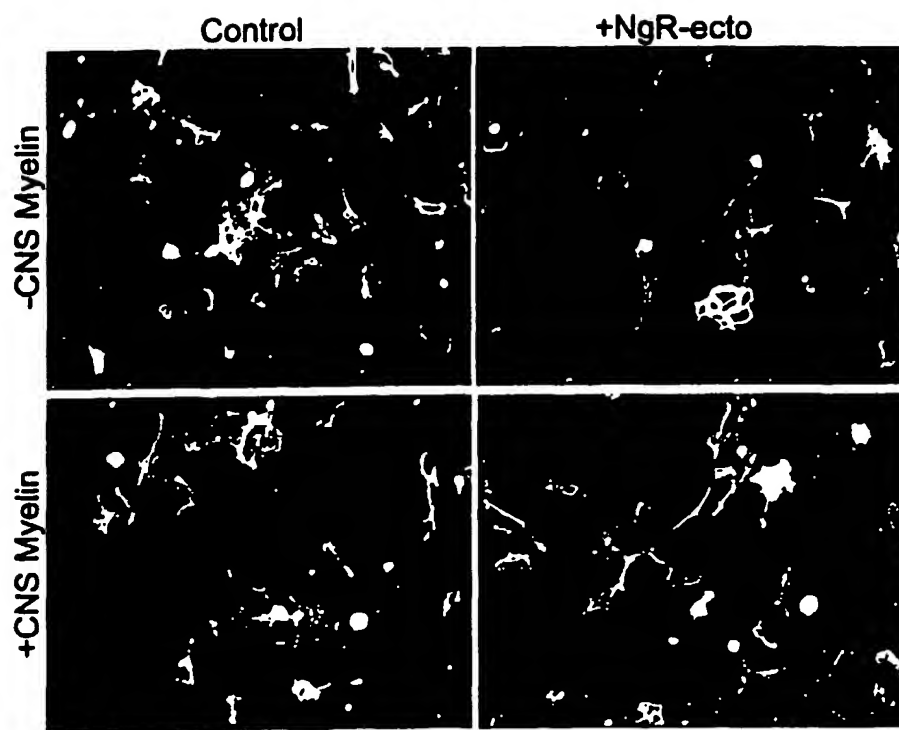


FIG. 11a

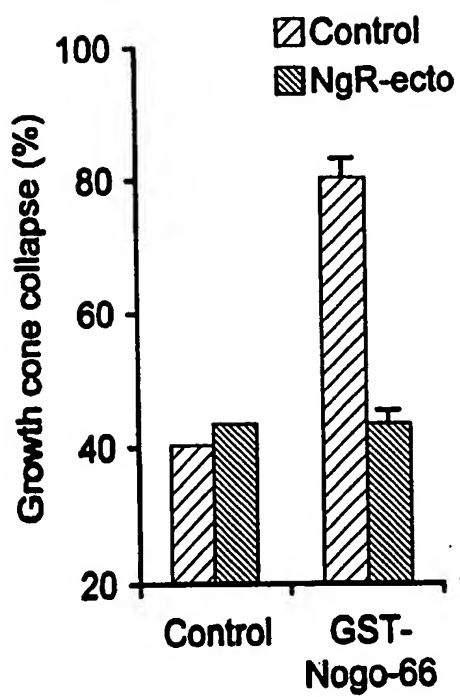
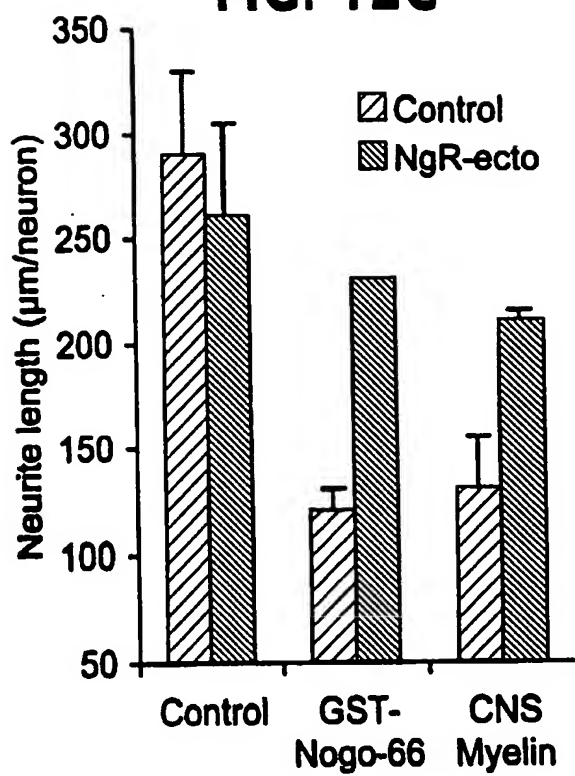


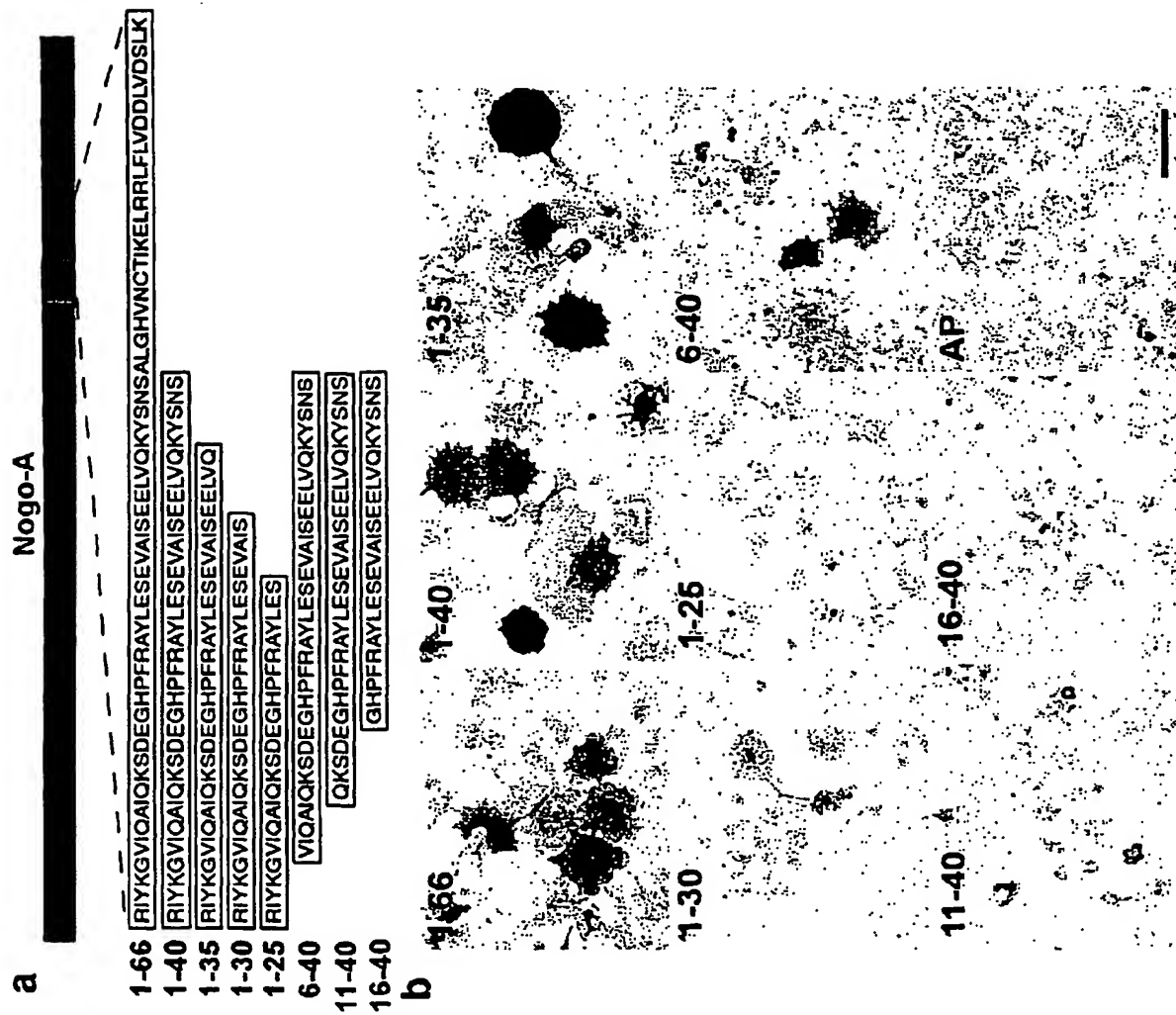
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FIG. 12A



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**FIG. 12B****FIG. 12C**

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FIG. 13

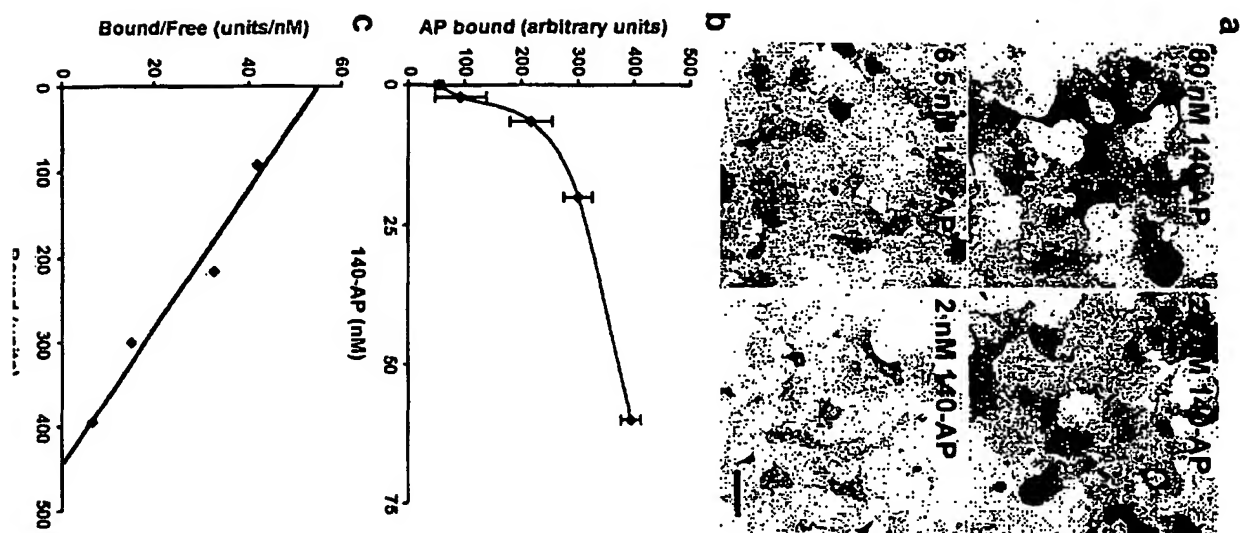
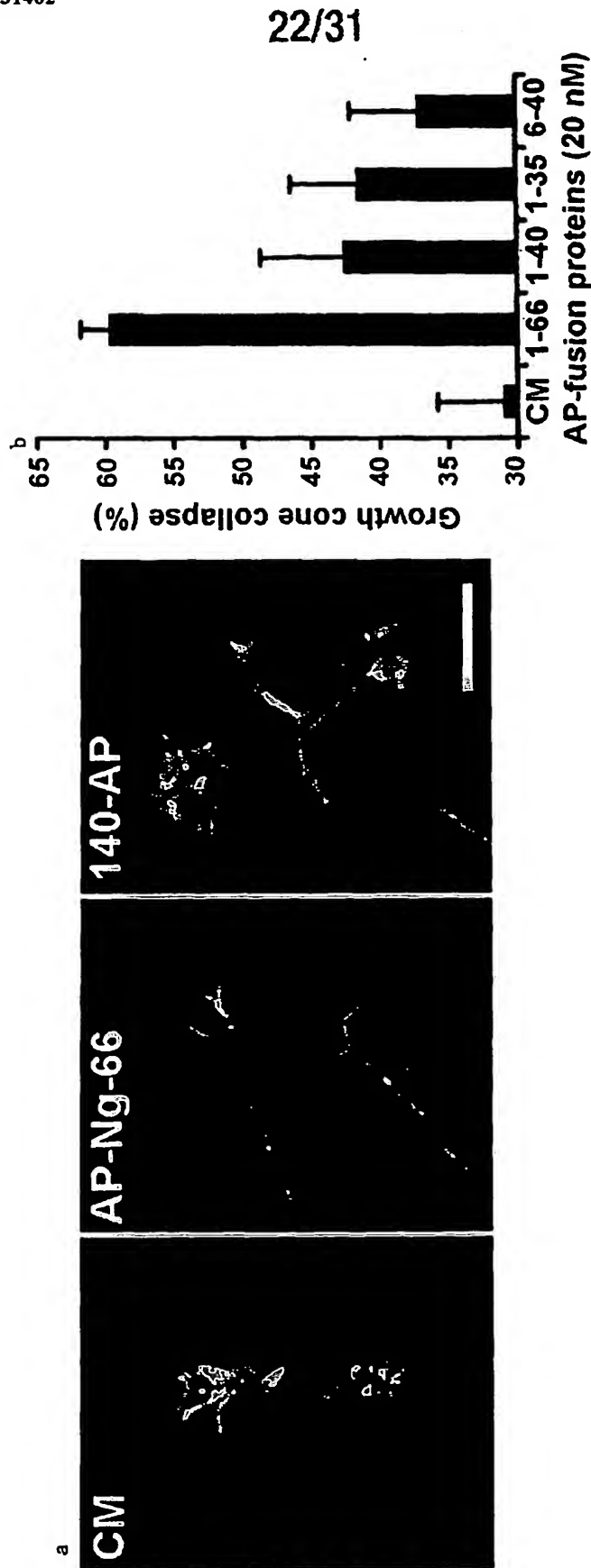
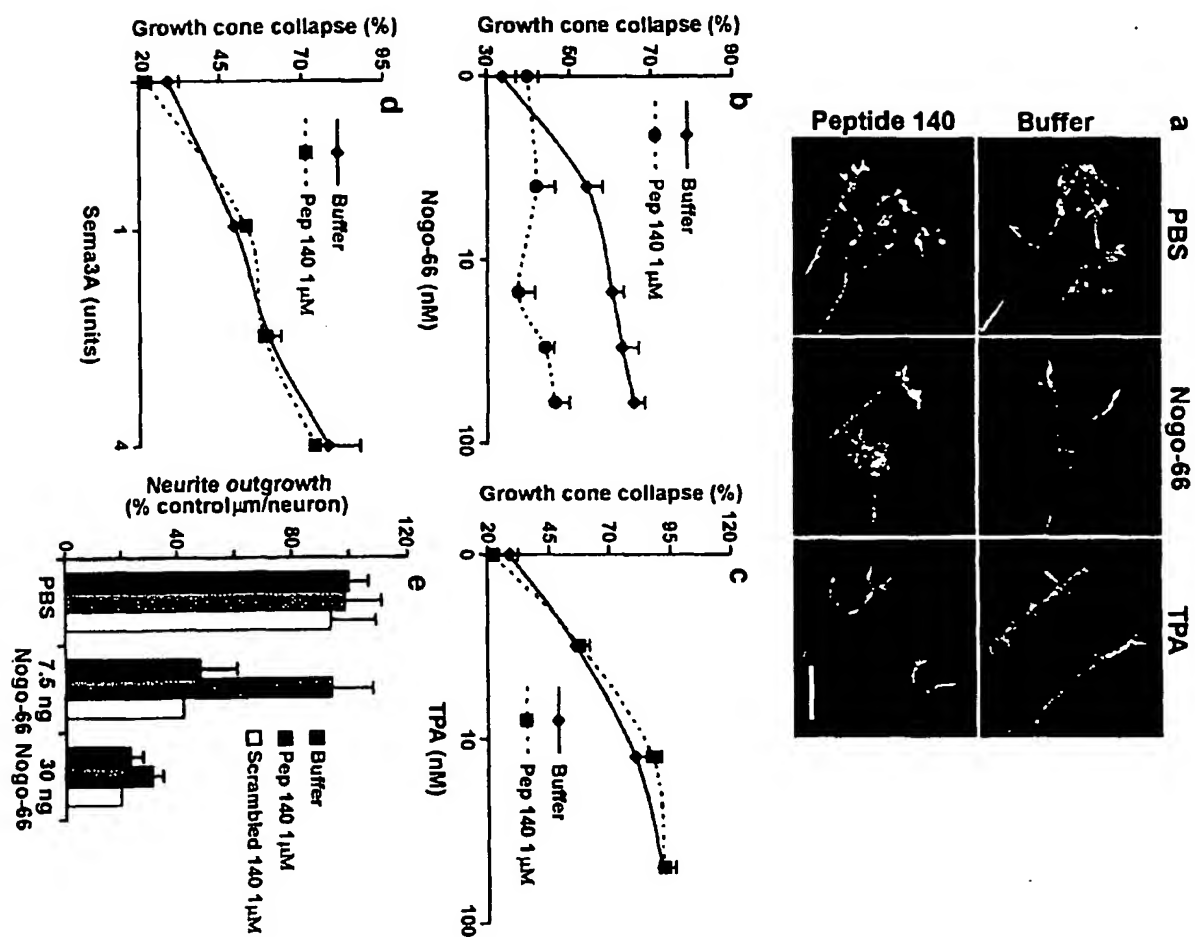
21/31  
FIG. 14

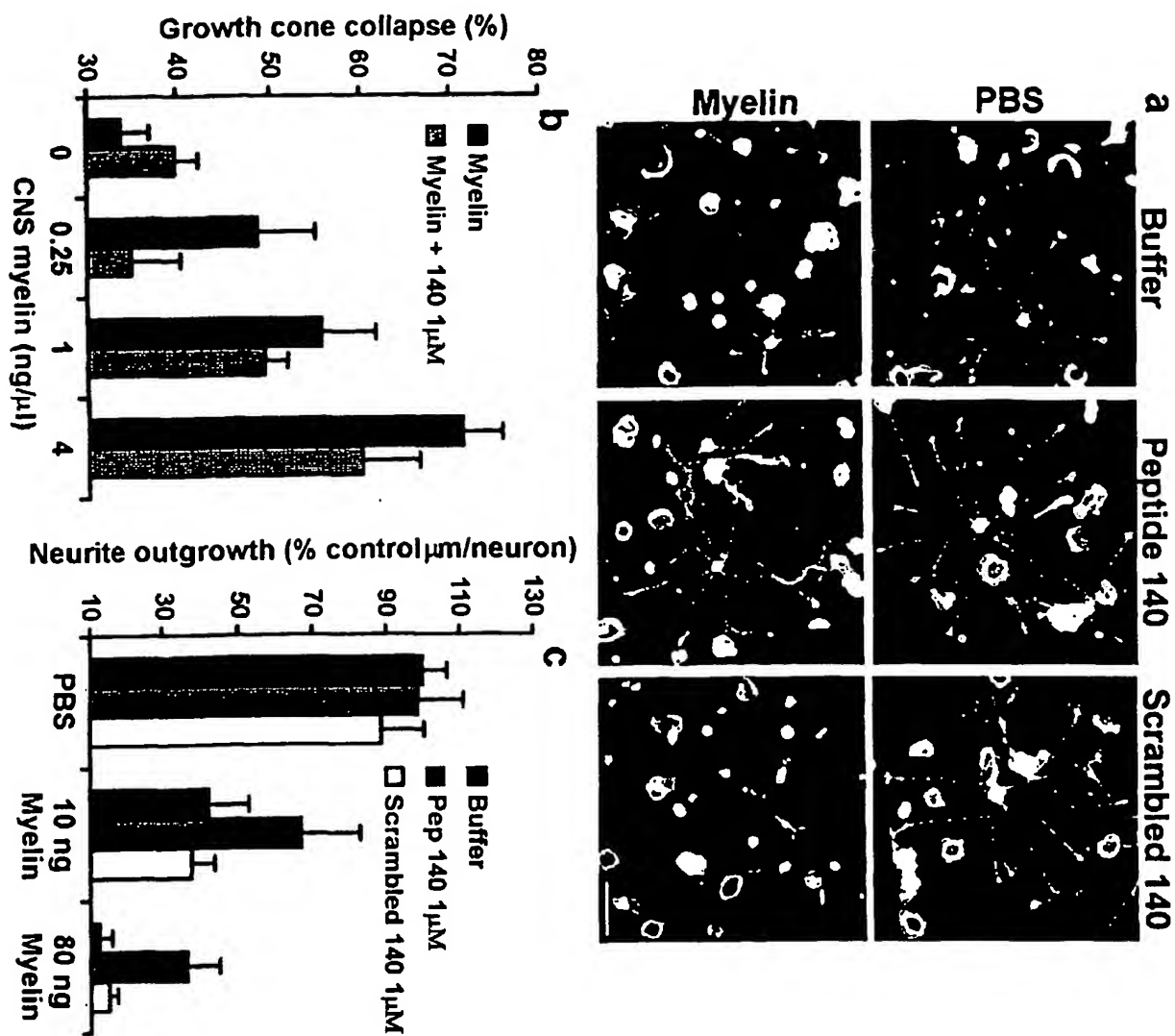


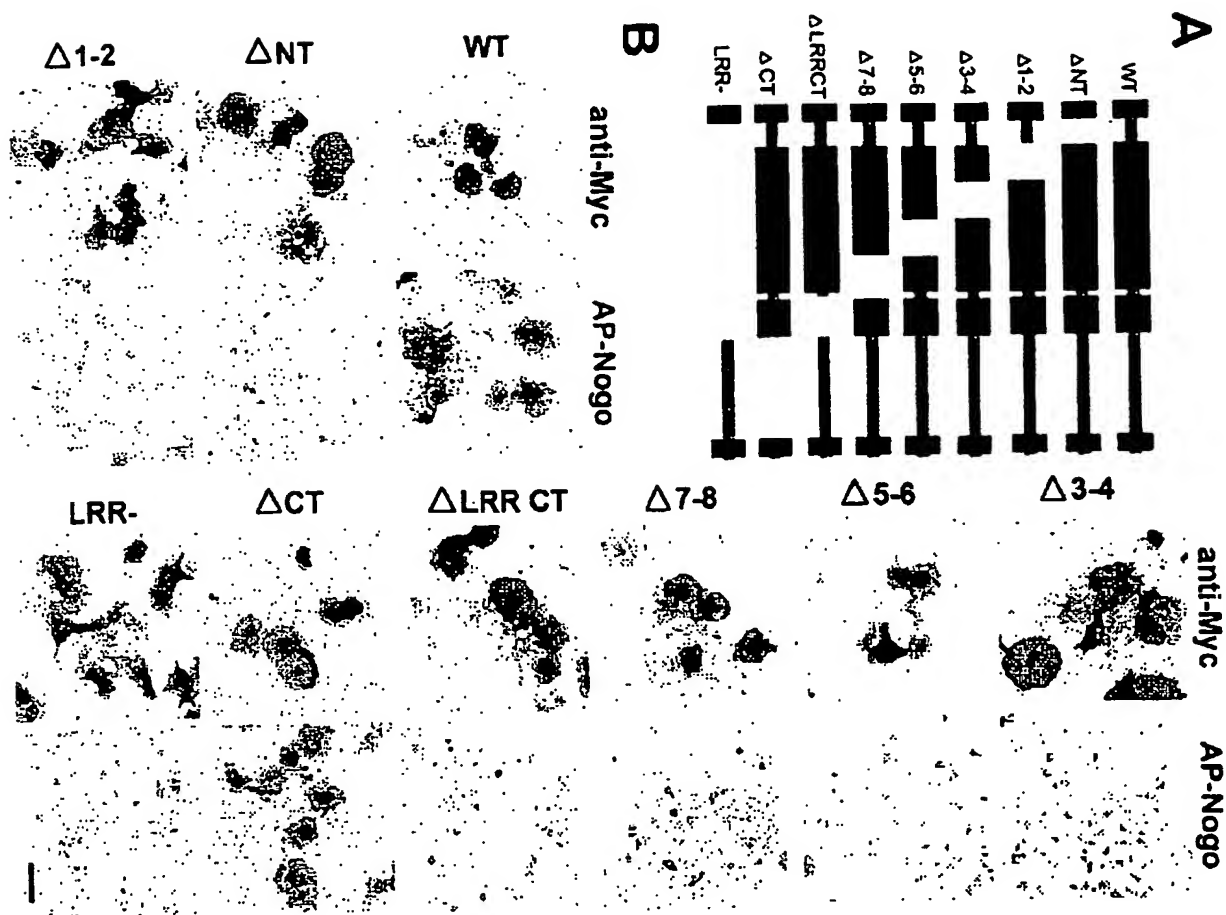
FIG. 15



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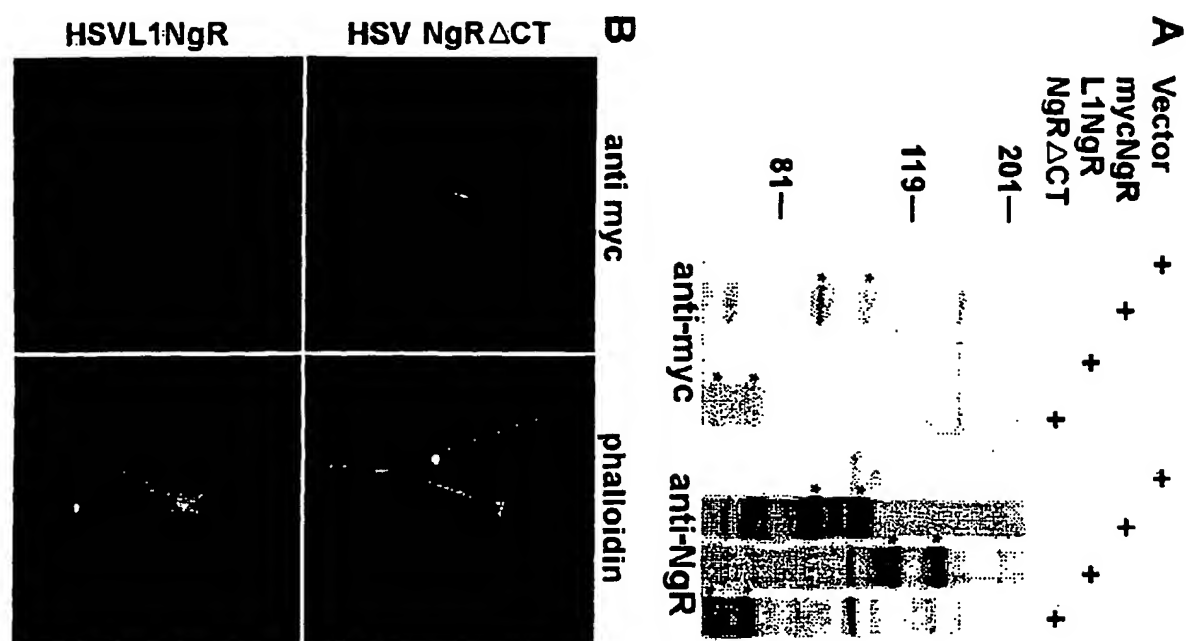
23/31  
FIG. 16

24/31  
FIG. 17

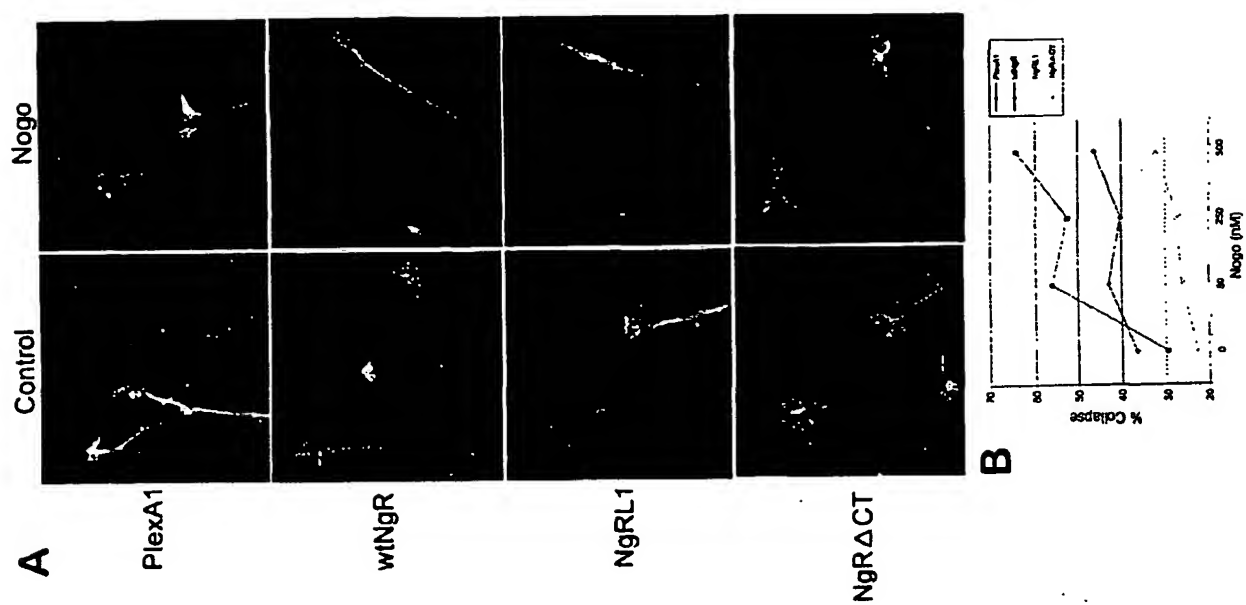
25/31  
FIG. 18

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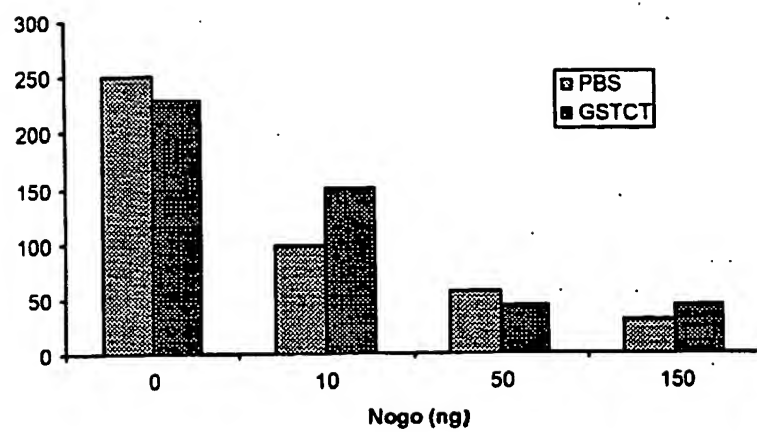
26/31  
FIG. 19



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27/31  
FIG. 20

28/31  
FIG. 21



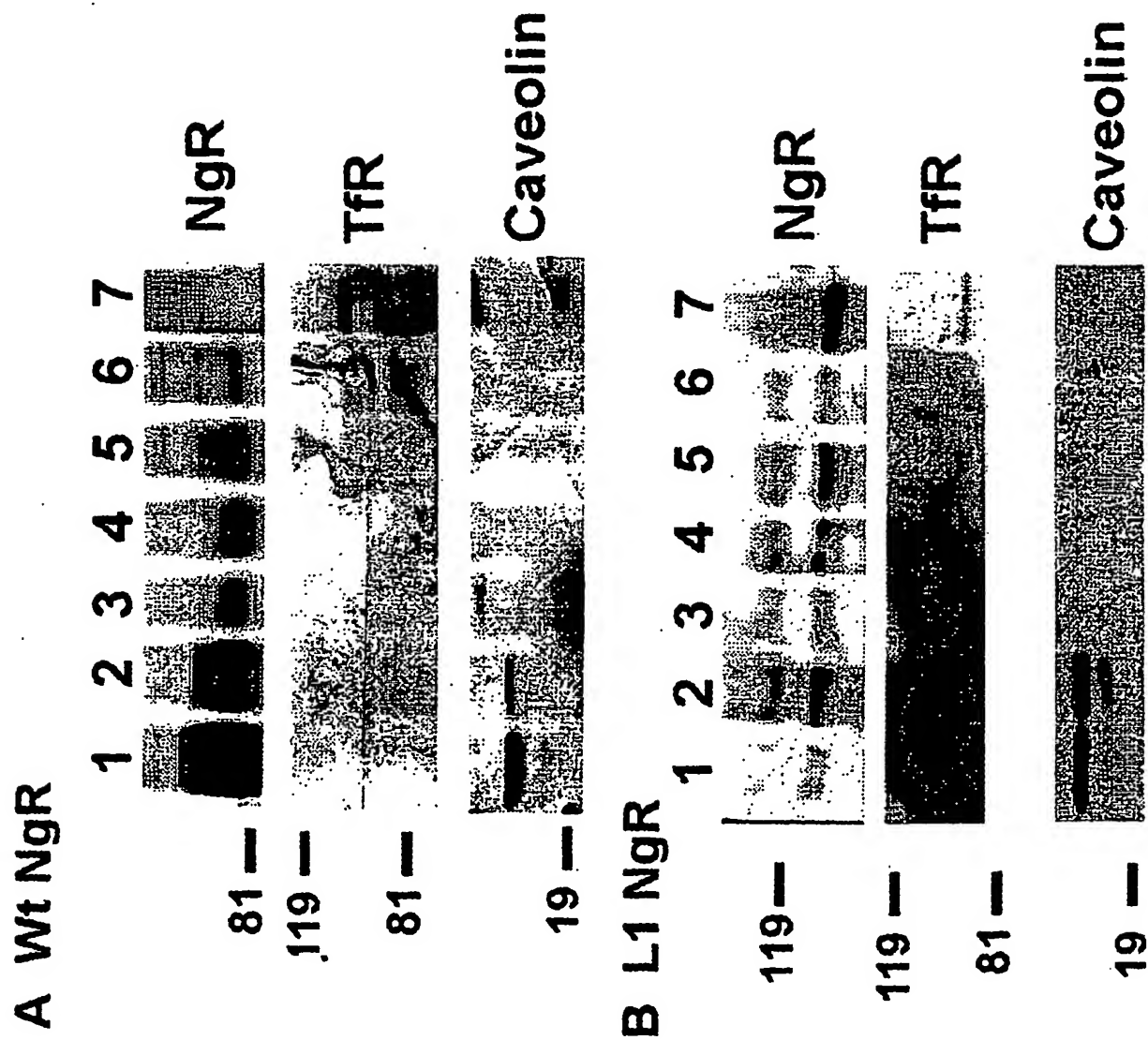
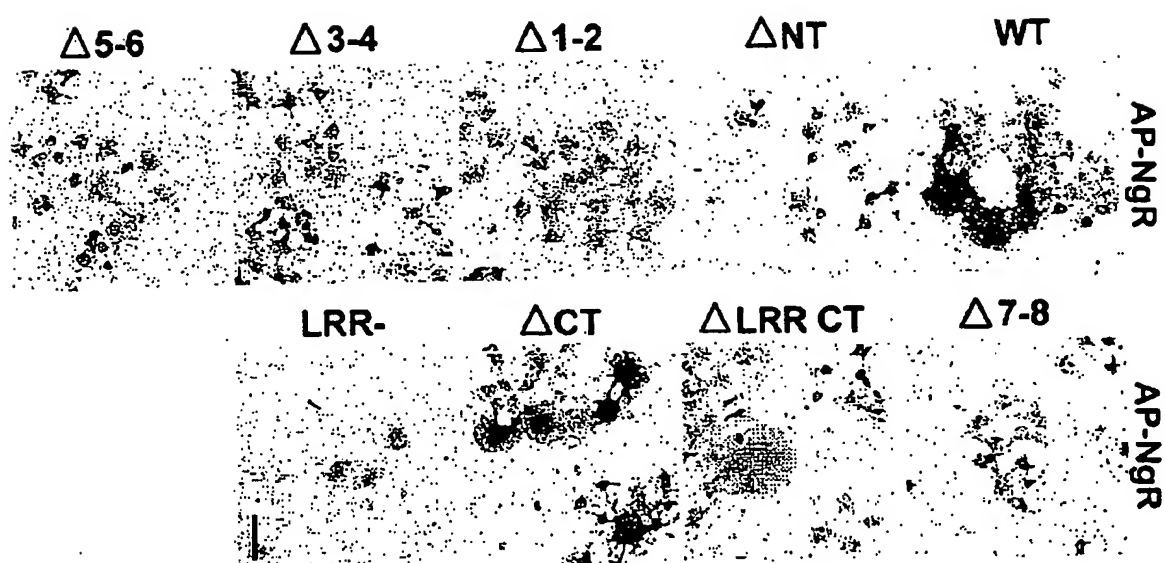


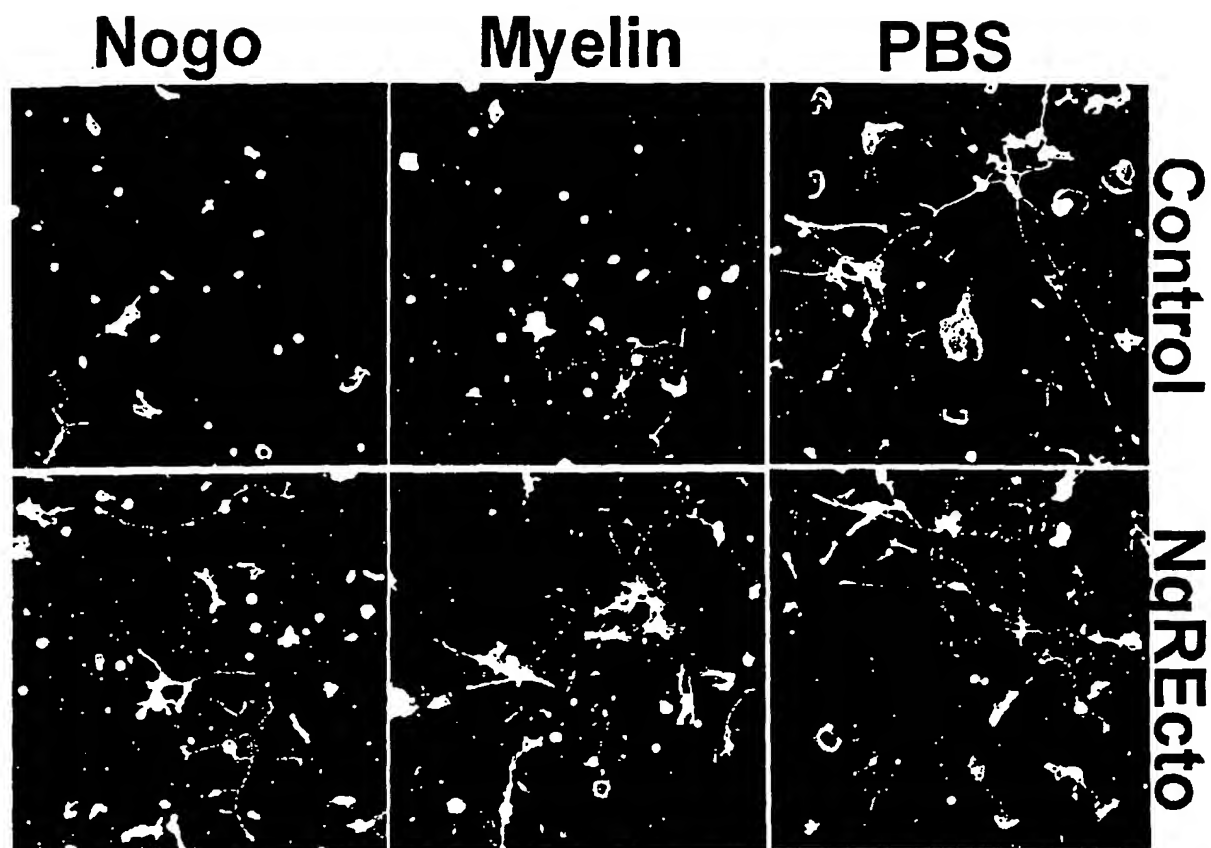
FIG. 22



30/31  
FIG. 23



BEST AVAILABLE COPY

31/31  
FIG. 24

## SEQUENCE LISTING

&lt;110&gt; Yale University

&lt;120&gt; NOGO RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

&lt;130&gt; C077 CIP PCT

&lt;140&gt; Not yet assigned

&lt;141&gt; 2002-10-04

&lt;150&gt; 09/972,599

&lt;151&gt; 2001-10-06

&lt;160&gt; 57

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1719

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (166)..(1584)

&lt;223&gt; Predicted human Nogo receptor gene

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ccgaaacgac tttagtccc cgacgcgccc cgcccaaccc ctacg atg aag agg gcg 177  
Met Lys Arg Ala

1

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Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val Leu Trp Leu Gln Ala  
5 10 15 20tgg cag gtg gca gcc cca tgc cca ggt gcc tgc gta tgc tac aat gag 273  
Trp Gln Val Ala Ala Pro Cys Pro Gly Ala Cys Val Cys Tyr Asn Glu  
25 30 35ccc aag gtg acg aca agc tgc ccc cag cag ggc ctg cag gct gtg ccc 321  
Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu Gln Ala Val Pro  
40 45 50gtg ggc atc cct gct gcc agc cag cgc atc ttc ctg cac ggc aac cgc 369  
Val Gly Ile Pro Ala Ala Ser Gln Arg Ile Phe Leu His Gly Asn Arg  
55 60 65atc tgc cat gtg cca gct gcc agc ttc cgt gcc tgc cgc aac ctc acc 417  
Ile Ser His Val Pro Ala Ala Ser Phe Arg Ala Cys Arg Asn Leu Thr  
70 75 80atc ctg tgg ctg cac tgc aat gtg ctg gcc cga att gat gcg gct gcc 465  
Ile Leu Trp Leu His Ser Asn Val Leu Ala Arg Ile Asp Ala Ala Ala  
85 90 95 100ttc act ggc ctg gcc ctc ctg gag cag ctg gac ctc agc gat aat gca 513  
Phe Thr Gly Leu Ala Leu Leu Glu Gln Leu Asp Leu Ser Asp Asn Ala  
105 110 115

cag ctc cgg tct gtg gac cct gcc aca ttc cac ggc ctg ggc cgc cta	561
Gln Leu Arg Ser Val Asp Pro Ala Thr Phe His Gly Leu Gly Arg Leu	
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His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu Leu Gly Pro Gly	
135 140 145	
ctg ttc cgc ggc ctg gct gcc ctg cag tac ctc tac ctg cag gac aac	657
Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr Leu Gln Asp Asn	
150 155 160	
gcg ctg cag gca ctg cct gat gac acc ttc cgc gac ctg ggc aac ctc	705
Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp Leu Gly Asn Leu	
165 170 175 180	
aca cac ctc ttc ctg cac ggc aac cgc atc tcc agc gtg ccc gag cgc	753
Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser Val Pro Glu Arg	
185 190 195	
gcc ttc cgt ggg ctg cac agc ctc gac cgt ctc cta ctg cac cag aac	801
Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu Leu His Gln Asn	
200 205 210	
cgc gtg gcc cat gtg cac ccg cat gcc ttc cgt gac ctt ggc cgc ctc	849
Arg Val Ala His Val His Pro His Ala Phe Arg Asp Leu Gly Arg Leu	
215 220 225	
atg aca ctc tat ctg ttt gcc aac aat cta tca gcg ctg ccc act gag	897
Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala Leu Pro Thr Glu	
230 235 240	
gcc ctg gcc ccc ctg cgt gcc ctg cag tac ctg agg ctc aac gac aac	945
Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu Arg Leu Asn Asp Asn	
245 250 255 260	
ccc tgg gtg tgt gac tgc cgg gca cgc cca ctc tgg gcc tgg ctg cag	993
Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp Ala Trp Leu Gln	
265 270 275	
aag ttc cgc ggc tcc tcc tcc gag gtg ccc tgc agc ctc ccg caa cgc	1041
Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Ser Leu Pro Gln Arg	
280 285 290	
ctg gct ggc cgt gac ctc aaa cgc cta gct gcc aat gac ctg cag ggc	1089
Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Asn Asp Leu Gln Gly	
295 300 305	
tgc gct gtg gcc acc ggc cct tac cat ccc atc tgg acc ggc agg gcc	1137
Cys Ala Val Ala Thr Gly Pro Tyr His Pro Ile Trp Thr Gly Arg Ala	
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Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala	
325 330 335 340	
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Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly	
345 350 355	
aat gcg ctg aag gga cgc gtg ccg ccc ggt gac agc ccg ccg ggc aac	1281
Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn	
360 365 370	
ggc tct ggc cca cgg cac atc aat gac tca ccc ttt ggg act ctg cct	1329

Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro  
 375 380 385  
 ggc tct gct gag ccc ccg ctc act gca gtg cgg ccc gag ggc tcc gag 1377  
 Gly Ser Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu  
 390 395 400  
 cca cca ggg ttc ccc acc tcg ggc cct cgc cgg agg cca ggc tgt tca 1425  
 Pro Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser  
 405 410 415 420  
 cgc aag aac cgc acc cgc agc cac tgc cgt ctg ggc cag gca ggc agc 1473  
 Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser  
 425 430 435  
 ggg ggt ggc ggg act ggt gac tca gaa ggc tca ggt gcc cta ccc agc 1521  
 Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu Pro Ser  
 440 445 450  
 ctc acc tgc agc ctc acc ccc ctg ggc ctg gcg ctg gtg ctg tgg aca 1569  
 Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val Leu Trp Thr  
 455 460 465  
 gtg ctt ggg ccc tgc tgacccccag cggacacaag agcgtgctca gcagccaggt 1624  
 Val Leu Gly Pro Cys  
 470  
 gtgtgtacat acgggggtctc tctccacgcc gccaagccag ccggggcggcc gacccgtggg 1684  
 gcaggccagg ccaggtcctc cctgatggac gcctg 1719

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&lt;211&gt; 473

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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 Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu  
 35 40 45  
 Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile Phe Leu  
 50 55 60  
 His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg Ala Cys  
 65 70 75 80  
 Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala Arg Ile  
 85 90 95  
 Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Glu Gln Leu Asp Leu  
 100 105 110  
 Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe His Gly  
 115 120 125  
 Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu  
 130 135 140

Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr  
 145 150 155 160  
 Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp  
 165 170 175  
 Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser  
 180 185 190  
 Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu  
 195 200 205  
 Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp  
 210 215 220  
 Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala  
 225 230 235 240  
 Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu Arg  
 245 250 255  
 Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp  
 260 265 270  
 Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Ser  
 275 280 285  
 Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Asn  
 290 295 300  
 Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro Ile Trp  
 305 310 315 320  
 Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys Cys Cys  
 325 330 335  
 Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro  
 340 345 350  
 Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Ser  
 355 360 365  
 Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe  
 370 375 380  
 Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Val Arg Pro  
 385 390 395 400  
 Glu Gly Ser Glu Pro Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg  
 405 410 415  
 Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly  
 420 425 430  
 Gln Ala Gly Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly  
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 cgggcgccccg cccgaagcc gcttccagtg cccgacgcgc cccgctcgac cccgaag 177  
 atg aag agg gcg tcc tcc gga gga agc agg ctg ctg gca tgg gtg tta 225  
 Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu  
 1 5 10 15  
 tgg cta cag gcc tgg agg gta gca aca cca tgc cct ggt gct tgt gtg 273  
 Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val  
 20 25 30  
 tgc tac aat gag ccc aag gta aca aca agc tgc ccc cag cag ggt ctg 321  
 Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu  
 35 40 45  
 cag gct gtg ccc act ggc atc cca gcc tct agc cag cga atc ttc ctg 369  
 Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu  
 50 55 60  
 cat ggc aac cga atc tct cac gtg cca gct gcg agc ttc cag tca tgc 417  
 His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Gln Ser Cys  
 65 70 75 80  
 cga aat ctc act atc ctg tgg ctg cac tct aat gcg ctg gct cgg atc 465  
 Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Arg Ile  
 85 90 95  
 gat gct gct gcc ttc act ggt ctg acc ctc ctg gag caa cta gat ctt 513  
 Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu  
 100 105 110  
 agt gat aat gca cag ctt cat gtc gtg gac cct acc acg ttc cac ggc 561  
 Ser Asp Asn Ala Gln Leu His Val Val Asp Pro Thr Thr Phe His Gly  
 115 120 125  
 ctg ggc cac ctg cac aca ctg cac cta gac cga tgt ggc ctg cgg gag 609  
 Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Arg Glu  
 130 135 140  
 ctg ggt ccc ggc cta ttc cgt gga cta gca gct ctg cag tac ctc tac 657  
 Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr  
 145 150 155 160  
 cta caa gac aac aat ctg cag gca ctc cct gac aac acc ttt cga gac 705  
 Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp  
 165 170 175  
 ctg ggc aac ctc acg cat ctc ttt ctg cat ggc aac cgt atc ccc agt 753  
 Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser  
 180 185 190

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Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu	
195 200 205	
ttg cac cag aac cat gtg gct cgt gtg cac cca cat gcc ttc cgg gac	849
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp	
210 215 220	
ctt ggc cgc ctc atg acc ctc tac ctg ttt gcc aac aac ctc tcc atg	897
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met	
225 230 235 240	
ctg cct gca gag gtc cta atg ccc ctg agg tct ctg cag tac ctg cga	945
Leu Pro Ala Glu Val Leu Met Pro Leu Arg Ser Leu Gln Tyr Leu Arg	
245 250 255	
ctc aat gac aac ccc tgg gtg tgt gac tgc cgg gca cgt cca ctc tgg	993
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp	
260 265 270	
gcc tgg ctg cag aag ttc cga ggt tcc tca tca gag gtg ccc tgc aac	1041
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn	
275 280 285	
ctg ccc caa cgc ctg gca gac cgt gat ctt aag cgc ctc gct gcc agt	1089
Leu Pro Gln Arg Leu Ala Asp Arg Asp Leu Lys Arg Leu Ala Ala Ser	
290 295 300	
gac cta gag ggc tgt gct gtg gct tca gga ccc ttc cgt ccc atc cag	1137
Asp Leu Glu Gly Cys Ala Val Ala Ser Gly Pro Phe Arg Pro Ile Gln	
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Thr Ser Gln Leu Thr Asp Glu Glu Leu Leu Ser Leu Pro Lys Cys Cys	
325 330 335	
cag cca gat gct gca gac aaa gcc tca gta ctg gaa ccc ggg agg cca	1233
Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro	
340 345 350	
gct tct gcc gga aac gcc ctc aag gga cgt gtg cct ccc ggt gac act	1281
Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr	
355 360 365	
cca cca ggc aat ggc tca ggc cct cgg cac atc aat gac tct cca ttt	1329
Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe	
370 375 380	
gga act ttg ccc agc tct gca gag ccc cca ctg act gcc ctg cgg cct	1377
Gly Thr Leu Pro Ser Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro	
385 390 395 400	
ggg ggt tcc gag cca cca gga ctt ccc acc act ggt ccc cgc agg agg	1425
Gly Gly Ser Glu Pro Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg	
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Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly	
420 425 430	
cag gcg gga agt ggg gcc agt gga aca ggg gac gca gag ggt tca ggg	1521
Gln Ala Gly Ser Gly Ala Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly	
435 440 445	
gct ctg cct gct ctg gcc tgc agc ctt gct cct ctg ggc ctt gca ctg	1569



Ala Leu Pro Ala Leu Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu  
 450 455 460

gta ctt tgg aca gtg ctt ggg ccc tgc tgaccagcca ccagccacca 1616  
 Val Leu Trp Thr Val Leu Gly Pro Cys  
 465 470

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aggggcaggc caggccctcc ctgacagatg cctccccacc agcccacccc catctccacc 1736

ccatcatgtt tacagggttc cgggggtggc ggttggttca caacccaac ttccaccgg 1796

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ataaacagct 1866

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 35 40 45

Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu  
 50 55 60

His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Gln Ser Cys  
 65 70 75 80

Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Arg Ile  
 85 90 95

Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu  
 100 105 110

Ser Asp Asn Ala Gln Leu His Val Val Asp Pro Thr Thr Phe His Gly  
 115 120 125

Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Arg Glu  
 130 135 140

Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr  
 145 150 155 160

Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp  
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Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu  
 195 200 205

Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp  
 210 215 220

Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met  
 225 230 235 240  
 Leu Pro Ala Glu Val Leu Met Pro Leu Arg Ser Leu Gln Tyr Leu Arg  
 245 250 255  
 Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp  
 260 265 270  
 Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn  
 275 280 285  
 Leu Pro Gln Arg Leu Ala Asp Arg Asp Leu Lys Arg Leu Ala Ala Ser  
 290 295 300  
 Asp Leu Glu Gly Cys Ala Val Ala Ser Gly Pro Phe Arg Pro Ile Gln  
 305 310 315 320  
 Thr Ser Gln Leu Thr Asp Glu Glu Leu Leu Ser Leu Pro Lys Cys Cys  
 325 330 335  
 Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro  
 340 345 350  
 Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr  
 355 360 365  
 Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe  
 370 375 380  
 Gly Thr Leu Pro Ser Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro  
 385 390 395 400  
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 405 410 415  
 Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly  
 420 425 430  
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&lt;210&gt; 5

&lt;211&gt; 4053

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (135)..(3710)

 <223> Human DNA encoding for Nogo protein (K1AA0886, GenBank  
 Accession No. AB020693)

&lt;400&gt; 5

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      1          5          10

tcg gac agc cca ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg 218
Ser Asp Ser Pro Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val
      15          20          25

agg gag ccc gag gac gag gag gaa gaa gag gag gag gaa gag gag gac 266
Arg Glu Pro Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp
      30          35          40

gag gac gaa gac ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc 314
Glu Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala
      45          50          55          60

gcc ggg ctg tcc gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg 362
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ccc ctg atg gac ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga 410
Pro Leu Met Asp Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly
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ccc ctg ccg gcc gct ccc ccc gtc gcc ccg gag ccg cag ccg tct tgg 458
Pro Leu Pro Ala Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp
      95          100          105

gac ccg agc ccg gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct 506
Asp Pro Ser Pro Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser
      110          115          120

gct gcc gca gtc tcg ccc tcc aag ctc cct gag gac gac gag cct ccg 554
Ala Ala Ala Val Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro
      125          130          135          140

gcc ccg cct ccc cct cct ccc ccg gcc agc gtg agc ccc cag gca gag 602
Ala Arg Pro Pro Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu
      145          150          155

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Pro Val Trp Thr Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr
      160          165          170

ccg gcc gcg ccc aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc 698
Pro Ala Ala Pro Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr
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ctt ttt gct ctt cct gct gca tct gag cct gtg ata cgc tcc tct gca 746
Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala
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Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly
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Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
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tct ctg tct cct ctc tca gcc gct tct ttc aaa gaa cat gaa tac ctt 890
Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu
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gtc agt gaa gct tct aaa gag gtc tca gag aag gca aaa act cta ctc	986
Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu	
270 275 280	
ata gat aga gat tta aca gag ttt tca gaa tta gaa tac tca gaa atg	1034
Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met	
285 290 295 300	
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Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val	
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gca aat cct agg gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag	1130
Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu	
320 325 330	
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Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr	
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gct ctt act aaa ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa	1226
Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys	
350 355 360	
gca aaa gac agt ttt aat gaa aag aga gtt gca gtg gaa gct cct atg	1274
Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met	
365 370 375 380	
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Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val	
385 390 395	
aaa gat agt aag gaa gat agt gat atg ttg gct gct gga ggt aaa atc	1370
Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile	
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Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser	
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Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp	
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Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala	
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Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala	
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aca aac att ttt cct ttg tta gga gat cct act tca gaa aat aag acc	1610
Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr	
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Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln	
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560 565 570	
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Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu	
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Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu	
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Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu	
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Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser	
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Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu	
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Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys	
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Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn	
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Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser	
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Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val	
750 755 760	
atg ctt gtg aaa gaa agt ctc act gag act tca ttt gag tca atg ata	2474

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				785					790					795		
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	845				850				855						860	
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Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp			
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Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn			
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Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val			
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Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly			
1120	1125	1130	
gcc ttg ttt aat ggt ctg aca cta ctg att ttg gct ctc att tca ctc			3578
Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu			
1135	1140	1145	
ttc agt gtt cct gtt att tat gaa cgg cat cag gca cag ata gat cat			3626
Phe Ser Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His			
1150	1155	1160	
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Tyr Leu Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile			
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Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu			
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&lt;210&gt; 6

&lt;211&gt; 1192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp	
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Phe	Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala	
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Ala	Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Asp	Pro	Ser	Pro	
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Val	Ser	Ser	Thr	Val	Pro	Ala	Pro	Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val	
115					120					125						
Ser	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	
130					135					140						
Pro	Pro	Pro	Pro	Ala	Ser	Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr	
145					150					155					160	
Pro	Pro	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro	
165					170					175						
Lys	Arg	Arg	Gly	Ser	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	Phe	Ala	Leu	
180					185					190						
Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Arg	Ser	Ser	Ala	Glu	Asn	Met	Asp	
195					200					205						
Leu	Lys	Glu	Gln	Pro	Gly	Asn	Thr	Ile	Ser	Ala	Gly	Gln	Glu	Asp	Phe	
210					215					220						
Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro	
225					230					235					240	
Leu	Ser	Ala	Ala	Ser	Phe	Lys	Glu	His	Glu	Tyr	Leu	Gly	Asn	Leu	Ser	
245					250					255						
Thr	Val	Leu	Pro	Thr	Glu	Gly	Thr	Leu	Gln	Glu	Asn	Val	Ser	Glu	Ala	
260					265					270						
Ser	Lys	Glu	Val	Ser	Glu	Lys	Ala	Lys	Thr	Leu	Leu	Ile	Asp	Arg	Asp	
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Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly	Ser	Ser	Phe	
290					295					300						
Ser	Val	Ser	Pro	Lys	Ala	Glu	Ser	Ala	Val	Ile	Val	Ala	Asn	Pro	Arg	
305					310					315					320	
Glu	Glu	Ile	Ile	Val	Lys	Asn	Lys	Asp	Glu	Glu	Glu	Lys	Leu	Val	Ser	
325					330					335						
Asn	Asn	Ile	Leu	His	Asn	Gln	Gln	Glu	Leu	Pro	Thr	Ala	Leu	Thr	Lys	
340					345					350						
Leu	Val	Lys	Glu	Asp	Glu	Val	Val	Ser	Ser	Glu	Lys	Ala	Lys	Asp	Ser	
355					360					365						



Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr  
 370 375 380  
 Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys  
 385 390 395 400  
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 Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr  
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 Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro  
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 465 470 475 480  
 Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys  
 485 490 495  
 Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr  
 500 505 510  
 Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp  
 515 520 525  
 Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala  
 530 535 540  
 Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu  
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 Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys  
 565 570 575  
 Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro  
 580 585 590  
 Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser  
 595 600 605  
 Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val  
 610 615 620  
 Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu  
 625 630 635 640  
 Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro  
 645 650 655  
 Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly  
 660 665 670  
 Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln  
 675 680 685  
 Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu  
 690 695 700  
 Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu  
 705 710 715 720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu  
 725 730 735  
 Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser  
 740 745 750  
 Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys  
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 770 775 780  
 Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu  
 785 790 795 800  
 Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro  
 805 810 815  
 Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met  
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 Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp  
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 Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His  
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 900 905 910  
 Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val  
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 Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu  
 995 1000 1005  
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 1010 1015 1020  
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 1025 1030 1035 1040  
 Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile  
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 Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro

1060	1065	1070
Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val 1075	1080	1085
Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys 1090	1095	1100
Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys 1105	1110	1115 1120
Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn 1125	1130	1135
Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro 1140	1145	1150
Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu 1155	1160	1165
Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile 1170	1175	1180
Pro Gly Leu Lys Arg Lys Ala Glu 1185	1190	

<210> 7  
 <211> 75  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: cDNA encoding  
 receptor binding inhibitor Pep 1

<400> 7  
 tttaggatat acaagggtgt gatccaagct atccagaaat cagatgaagg ccacccattc 60  
 agggcatatc tggaa 75

<210> 8  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pep1- Nogo  
 protein inhibitor

<400> 8  
 Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu  
 1 5 10 15  
 Gly His Pro Phe Arg Ala Tyr Leu Glu  
 20 25

<210> 9  
 <211> 75  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA encoding  
receptor binding inhibitor Pep2

<400> 9  
atccagaaat cagatgaagg ccaccattc agggcatatc tggaatctga agttgctata 60  
tctgaggagt tgggt 75

<210> 10  
<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Pep2- Nogo  
protein inhibitor

<400> 10  
Ile Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser  
1 5 10 15  
Glu Val Ala Ile Ser Glu Glu Leu Val  
20 25

<210> 11  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: cDNA encoding  
receptor binding inhibitor Pep3

<400> 11  
agggcatatc tggaatctga agttgctata tctgaggagt tgggtcagaa gtacagtaat 60  
tctgctcttg gtc 75

<210> 12  
<211> 25  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Pep3- Nogo  
protein inhibitor

<400> 12  
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln  
1 5 10 15  
Lys Tyr Ser Asn Ser Ala Leu Gly His  
20 25

<210> 13  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: cDNA encoding  
receptor binding inhibitor Pep4

<400> 13  
 tctgaggagt tgggttcagaa gtacagtaat tctgctcttg gtcattgtgaa ctgcacgata 60  
 aaggaaactca ggcgc 75

<210> 14  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pep4- Nogo  
 protein inhibitor

<400> 14  
 Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val  
 1 5 10 15  
 Asn Cys Thr Ile Lys Glu Leu Arg Arg  
 20 25

<210> 15  
 <211> 75  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: cDNA encoding  
 receptor binding inhibitor Pep5

<400> 15  
 gctcttgggc atgtgaactg cagcagaaag gaactcaggc gcctcttctt agttgatgat 60  
 ttagttgatt ctctg 75

<210> 16  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pep5- Nogo  
 protein inhibitor

<400> 16  
 Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe  
 1 5 10 15  
 Leu Val Asp Asp Leu Val Asp Ser Leu  
 20 25

<210> 17  
 <211> 120  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: cDNA encoding  
 receptor binding inhibitor Pep2-41

<400> 17  
 aggatataca aggggtgtgat ccaagctatc cagaaatcag atgaaggcca cccattcagg 60  
 gcatactctgg aatctgaagt tgctatatct gaggagttgg ttcagaagta cagtaattct 120

<210> 18  
 <211> 40  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pep2-41- Nogo  
 protein inhibitor

<400> 18  
 Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
 1 5 10 15  
 His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu  
 20 25 30  
 Leu Val Gln Lys Tyr Ser Asn Ser  
 35 40

<210> 19  
 <211> 198  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(198)  
 <223> Full receptor binding region of Nogo gene

<400> 19  
 ttt agg ata tac aag ggt gtg atc caa gct atc cag aaa tca gat gaa 48  
 Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu  
 1 5 10 15  
 ggc cac cca ttc agg gca tat ctg gaa tct gaa gtt gct ata tct gag 96  
 Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu  
 20 25 30  
 gag ttg gtt cag aag tac agt aat tct gct ctt ggt cat gtg aac tgc 144  
 Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys  
 35 40 45  
 acg ata aag gaa ctc agg cgc ctc ttc tta gtt gat gat tta gtt gat 192  
 Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp  
 50 55 60  
 tct ctg 198  
 Ser Leu  
 65

<210> 20  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu  
 1 5 10 15  
 Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu  
 20 25 30

Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys  
                   35                                  40                                  45

Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp  
           50                                  55                                  60

Ser Leu  
   65

<210> 21  
 <211> 198  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Nucleotide sequence encoding amino acids 1055-1120  
       of human NogoA

<400> 21  
 aggatataca aggggtgtgat ccaagctatc cagaaatcag atgaaggcca ccatttcagg 60  
 gcatatctgg aatctgaagt tgctatatct gaggagtgg ttcagaagta cagtaattct 120  
 gctcttggtc atgtgaactg cacgataaag gaactcaggc gcctcttctt agttgatgat 180  
 ttagttgatt ctctgaag  198

<210> 22  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
   1                                  5                                  10                                  15

His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu  
                   20                                  25                                  30

Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr  
           35                                  40                                  45

Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser  
           50                                  55                                  60

Leu Lys  
   65

<210> 23  
 <211> 75  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Nucleotide sequence encoding amino acids 1055-1079  
       of human NogoA

<400> 23  
 aggatataca aggggtgtgat ccaagctatc cagaaatcag atgaaggcca ccatttcagg 60  
 gcatatctgg aatct  75

<210> 24

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
 1 5 10 15

His Pro Phe Arg Ala Tyr Leu Glu Ser  
 20 25

&lt;210&gt; 25

&lt;211&gt; 90

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Nucleotide sequence encoding amino acids 1055-1084  
 of human NogoA

&lt;400&gt; 25

aggatataca aggggtgtgat ccaagctatc cagaaatcag atgaaggcca cccattcagg 60  
 gcatactctgg aatctgaagt tgctatatct 90

&lt;210&gt; 26

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
 1 5 10 15

His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Ser Val Ala Ile Ser  
 20 25 30

&lt;210&gt; 27

&lt;211&gt; 105

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Nucleotide sequence encoding amino acids 1055-1089  
 of human NogoA

&lt;400&gt; 27

aggatataca aggggtgtgat ccaagctatc cagaaatcag atgaaggcca cccattcagg 60  
 gcatactctgg aatctgaagt tgctatatct gaggagtgg ttcag 105

&lt;210&gt; 28

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly  
 1 5 10 15

His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Ser Val Ala Ile Ser Glu  
 20 25 30



Glu Leu Val Gln  
35

<210> 29  
<211> 105  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Nucleotide sequence encoding amino acids 1060-1094  
of human NogoA

<400> 29  
gtgatccaag ctatccagaa atcagatgaa ggccacccat tcagggcata tctggaatct 60  
gaagttgcta tatctgagga gttggttcag aagtacagta attct 105

<210> 30  
<211> 36  
<212> PRT  
<213> Homo sapiens

<400> 30  
Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala  
1 5 10 15  
Tyr Leu Glu Ser Glu Ser Val Ala Ile Ser Glu Glu Leu Val Gln Lys  
20 25 30

Tyr Ser Asn Ser  
35

<210> 31  
<211> 90  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Nucleotide sequence encoding amino acids 1065-1094  
of human NogoA

<400> 31  
cagaaatcag atgaaggcca cccattcagg gcatatctgg aatctgaagt tgctatatct 60  
gaggagttgg ttcagaagta cagtaattct 90

<210> 32  
<211> 31  
<212> PRT  
<213> Homo sapiens

<400> 32  
Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu  
1 5 10 15  
Ser Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser  
20 25 30

<210> 33  
<211> 75  
<212> DNA  
<213> Homo sapiens

&lt;220&gt;

<223> Nucleotide sequence encoding amino acids 1070-1094  
of human NogoA

&lt;400&gt; 33

ggccacccat tcagggcata tctggaatct gaagttgcta tatctgagga gttgggttcag 60  
aagtacagta attct 75

&lt;210&gt; 34

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Ser Val Ala Ile Ser  
1 5 10 15Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser  
20 25

&lt;210&gt; 35

&lt;211&gt; 75

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Nucleotide sequence encoding amino acids 1085-1109  
of human Noga

&lt;400&gt; 35

gaggagtggg ttcagaagta cagtaattct gctcttggtc atgtgaactg cagcataaag 60  
gaactcaggc gcctc 75

&lt;210&gt; 36

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn  
1 5 10 15Cys Thr Ile Lys Glu Leu Arg Arg Leu  
20 25

&lt;210&gt; 37

&lt;211&gt; 65

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 37

tgggatccga acaaaaactc atctcagaag aggatctgtc tagccagcga atcttcctgc 60  
atggc 65

&lt;210&gt; 38

&lt;211&gt; 32

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 38  
ttctcgaggt cagcagggcc caagcactgt cc 32

<210> 39  
<211> 62  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 39  
tgggatccga acaaaaactc atctcagaag aggatctgct agagggctgt gctgtggctt 60  
ca 62

<210> 40  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 40  
tgggatccga acaaaaactc atctcagaag aggatctgcc atgccctggt gcttgtgtgt 60  
gct 63

<210> 41  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 41  
ttgcggccgc tgaagccaca gcacagccct ctag 34

<210> 42  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 42  
ttgcggccgc tgagggttca ggggctctgc ctgct 35

<210> 43  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 43  
ggctgggatg ccagtgggca cagc 24

<210> 44  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 44  
ctcctggagc aactagatct tagt 24

<210> 45  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 45  
ggtcagacca gtgaaggcag cagc 24

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 46  
gctctgcagt acctctacct acaa 24

<210> 47  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 47  
tgctagtcca cggaataggc cggg 24

<210> 48  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 48  
agtcttgacc gcctcctctt gcac 24

<210> 49

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 49  
 gtgcaggcca cggaaagcgt gctc 24

<210> 50  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 50  
 tctctgcagt acctgcgact caat 24

<210> 51  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 51  
 gtggcttcag gacccttcg tcccatc 27

<210> 52  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 52  
 gtcattgagt cgcaggtact gcagagacct 30

<210> 53  
 <211> 137  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Residues 306-442 of human NogR1

<400> 53  
 Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro Ile Trp Thr  
 1 5 10 15  
 Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys Cys Cys Gln  
 20 25 30  
 Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro Ala  
 35 40 45

Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Ser Pro  
 50 55 60  
 Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly  
 65 70 75 80  
 Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu  
 85 90 95  
 Gly Ser Glu Pro Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro  
 100 105 110  
 Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln  
 115 120 125  
 Ala Gly Ser Gly Gly Gly Gly Thr Gly  
 130 135

&lt;210&gt; 54

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; Residues 306-473 of human NogoR1

&lt;400&gt; 54

Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro Ile Trp Thr  
 1 5 10 15  
 Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys Cys Cys Gln  
 20 25 30  
 Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro Ala  
 35 40 45  
 Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Ser Pro  
 50 55 60  
 Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly  
 65 70 75 80  
 Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu  
 85 90 95  
 Gly Ser Glu Pro Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro  
 100 105 110  
 Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln  
 115 120 125  
 Ala Gly Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala  
 130 135 140  
 Leu Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val  
 145 150 155 160  
 Leu Trp Thr Val Leu Gly Pro Cys  
 165

&lt;210&gt; 55

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; Residues 27-309 of human NogoR1

&lt;400&gt; 55

Cys Pro Gly Ala Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser  
 1 5 10 15  
 Cys Pro Gln Gln Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala  
 20 25 30  
 Ser Gln Arg Ile Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala  
 35 40 45  
 Ala Ser Phe Arg Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser  
 50 55 60  
 Asn Val Leu Ala Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu  
 65 70 75 80  
 Leu Glu Gln Leu Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser Val Asp  
 85 90 95  
 Pro Ala Thr Phe His Gly Leu Gly Arg Leu His Thr Leu His Leu Asp  
 100 105 110  
 Arg Cys Gly Leu Gln Glu Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala  
 115 120 125  
 Ala Leu Gln Tyr Leu Tyr Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro  
 130 135 140  
 Asp Asp Thr Phe Arg Asp Leu Gly Asn Leu Thr His Leu Phe Leu His  
 145 150 155 160  
 Gly Asn Arg Ile Ser Ser Val Pro Glu Arg Ala Phe Arg Gly Leu His  
 165 170 175  
 Ser Leu Asp Arg Leu Leu Leu His Gln Asn Arg Val Ala His Val His  
 180 185 190  
 Pro His Ala Phe Arg Asp Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe  
 195 200 205  
 Ala Asn Asn Leu Ser Ala Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg  
 210 215 220  
 Ala Leu Gln Tyr Leu Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys  
 225 230 235 240  
 Arg Ala Arg Pro Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser  
 245 250 255  
 Ser Glu Val Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu  
 260 265 270  
 Lys Arg Leu Ala Ala Asn Asp Leu Gln Gly Cys  
 275 280

&lt;210&gt; 56

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 56

Ile Tyr Lys Gly Val Ile Gln Ala Ile  
1 5

&lt;210&gt; 57

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 57

Glu Glu Leu Val  
1